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OM protein - protein search, using sw model

April 22, 2004, 17:51:09 ; Search time 50.1316 Seconds (without alignments) 2147.361 Million cell updates/sec Run on:

1 MSSRIARALALVVTLLHLTR.......ANEAAFPFYRLFNDIHKFRD 381 US-09-495-448A-4 2116 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:*
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geneseqp2003as:*
geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Aaw35730 Human cys	Human	7 Human	73 Human	61	38 Human	1107 Human	Human	Human	Abg76937 Human pro		ca.	Connec	Human	Human		Aar25565 Beta-IG-M	Aae05920 Mouse cys	5	m		m	1379 Rat	929	Adb25766 Mouse con
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ALIGNMENTS

AAW35730 standard; protein; 381 AA.

AAW35730;

(first entry) 27-MAR-1998 Human cysteine rich protein 61 (Cyr61)

Cysteine rich protein 61; Cyr61; human; extracellular matrix signalling molecule; cell adhesion; cell migration; cell proliferation; angiogenesis; chondrogenesis; oncogenesis; haematostasis; wound healing; organ regeneration.

Homo sapiens.

W09733995-A2

18-SEP-1997.

97WO-US004193. 14-MAR-1997; 96US-0013958P 15-MAR-1996;

(MUNI-) MUNIN CORP.

Lau LF;

WPI; 1997-470875/43. N-PSDB; AAT94699.

Isolated and purified cysteine rich protein 61, Cyr61 - useful to modulate e.g. haematostasis, induce wound healing, promote organ regeneration etc.

Claim 2; Page 112-113; 133pp; English.

This protein sequence comprises human cysteine rich protein 61 (Cyr61), an extracellular matrix signalling molecule. Its amino acid sequence was deduced from a human placental cDNA clone (see AA79469). Cyr61 cyr61 can be expressed in transformed or transfected host cells. Cyr61 can be used to modulate heematostamis, induce wound healing in a tissue, prochesis implantation, improve tissue graffing or promote for a modulator of angiogeneration, into a also be used to screen for a modulator of angiogenesis, chondrogenesis, oncogenesis, cell adhesion, cell migration, cell proliferation, expand a population of undifferentiated haematopoietic stem cells in culture and to screen for a

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2001-465561/50.
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                                                           N-PSDB; AAD11221
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mitogen (claimed). Ex vivo methods for using mammalian extracellular matrix signalling molecules to prepare blood products are also provided
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Pred. No. 8.9e-162;
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/note= "Cysteine free re
212. 281
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282. 381
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                                                         Similarity 100.
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                              Sequence 381 AA;
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The invention relates to extracellular matrix (ECM) signalling molecules involved in cellular response to growth factors. More particularly the involved in cellular response to growth factors. More particularly the involved in directed to cysteine-rich protein (Cyr61), and Cyr61-related proteins such as fibroblast secreted protein (Fispl2) and connective tissue growth factor (CTGP) and nucleic acid molecules encoding such proteins. The polypeptides of the invention are members of cysteine-rich secreted protein family. Human Cyr61 fragment is useful in methods for screening modulators of cell adhesion, cell migration, fibroblast cell prolaferation, angiogenesis, wound healing and Cyr61-integrin receptor interaction. Modulator of Cyr61-integrin alphavbeta3 interaction is used for the preparation of a medicament for the treatment of atherosclerosis, heart disease, tumour mecastasis, fibrosis, tumour growth, disorders associated with inadequate angiogenesis, aberrant granulation tissue development, abstrant fibroblast growth, and wounds. Polymcleotides of the invention are useful in gene therapy. The present sequence is human
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                                                                                                                                                                         Novel human cysteine-rich protein 61 (Cyr61) fragment useful in methods for screening for modulators of cell adhesion, fibroblast cell proliferation, angiogenesis and cell migration.
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100.0%; Pred. No. 8.9e-162;
ive 0; Mismatches 0;
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Greenspan JA;
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ô The present sequence represents a monocyte mature differentiation factor (MMDF) which maintains the life of macrophages for long periods in liquid culture. MMDF can be used as an anti-cancer agent, an immune activator and to treat infectious diseases 120 9 9 1 MSSRIARALALVVTLIHLTRIALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL NEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFOPNCQHQ Gaps term Human; monocyte; mature; differentiation factor; MMDF; macrophage; cancer; immune activator; tissue culture; infectious disease. - useful for the long ö Length 381; Indels Match
Local Similarity 99.5%; Pred. No. 5.6e-161;
es 379; Conservative 1; Mismatches 1; Human monocyte mature differentiation factor. A monocyte mature differentiation factor tissue culture of macrophage(s). Claim 9; Page 12-13; 22pp; Japanese. 96JP-00075236. 96JP-00075236. WPI; 1997-497320/46. Ä. N-PSDB; AAT97142 Sequence 381 AA; (TOYM) TOYOBO JP09234079-A. 04-MAR-1996; 04-MAR-1996; 09-SEP-1997. Query Match 61 Best Local Matches Ношо Ø 셤 ò ò

240 240 300 300 180 120 180 360 181 KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNMMIQSCKCNYNCP 61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNCKHO CICIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCREWVCDEDSIKDPMEDQDGLLG KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY 241 KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP HANEAAFPFYRLFNDIHKFRD 381 381 HANEAAFPFYRLFNDIHKFRD 301 181 241 301 361 361 121 셤 셤 g 셤 g 셤 ò 8 ò ò

RESULT 4
AAB90773
ID AAB90773 standard; protein; 381 AA.
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DT 15-JUN-2001 (first entry)

ò 240 240 120 120 180 300 300 360 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180 9 9 Human; shear stress-response protein; vascular disease; arteriosclerosis. of a l in the KELGFDASEVELTRNNELIAVGKGSSLKRLFVFGMEPRILYNPLQGGKCIVQTTSWSQCS 241 KTCGTGISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY 1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL CTCIDGAVGCIPLCFQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 181 KELGFDASEVELTRNNELIAVCKGRSLKRLPVFGKEPRIJNYPLOGOKCIVOTTSWSOCS AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP 241 KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY Gaps 1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 쏬 The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and Sakurada .; o sequences, proteins encoded by them and antibodies against in in diagnosis and treatment of vascular disease caused by Length 381; Indels Kawabata A, Query Match 99.5%; Score 2106; DB 4; Best Local Similarity 99.5%; Pred. No. 5.6e-161; Matches 379; Conservative 1; Mismatches 1; stress-response protein SEQ ID NO: , s, M, Ota' Sugano S Claim 60; Page 345-346; 678pp; Japanese. HANEAAFPFYRLFNDIHKFRD 381 H, Obayashi Nakamura Y, 02-OCT-2000; 2000WO-JP006840. 99JP-00280976 KOGYO KK (KYOW) KYOWA HAKKO (NOJI/) NOJIMA H. Yoshisue Sekine S, WPI; 2001-266308/27. N-PSDB; AAH02896. arteriosclerosis Sequence 381 AA; WO200125427-A1 01-OCT-1999; hypertension Homo sapiens 12-APR-2001 Nojima H, Kuga T, S 61 61 121 121 181 301 301 361 361 Human DNA 면 셤 ठे 요 à g ઠે ద ઠે 셤 ે 셤 ે ઠે

RESULT 5

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241 KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY 300
                                                                                                                                                                                                                  ABB05438 standard; protein; 381
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16-MAY-2001; 2001US-0291510P.
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N-PSDB; ABA93127, ABA93130.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of inhibiting proliferation of uterine leiomyoma or preventing uterine leiomyoma formation. The method comprises increasing the level of Cyfol in leiomyoma tissue. The invention also describes compounds and compositions that stimulate induction of the Cyfol gene and compounds that increase Cyfol activity. The compositions and the method of the invention are useful for preventing uterine leiomyoma formation or inhibiting proliferation of uterine leiomyoma in a subject. The method is particularly useful for treating or preventing uterine leiomyoma in a subject. The present sequence represents human Cyfol. Note: The present sequence represents human Cyfol. Note: The present sequence sequence order in the figure. The start of the sequence is shown on page 8/10 of the figures and the rest of the
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                                                                                                                                    Human; uterine leiomyoma proliferation; uterine leiomyoma formation;
Cyr61; cytostatic.
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Pred. No. 5.6e-161;
1; Mismatches 1; Indels (
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   AAU79761 standard; protein; 381 AA
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                                                                     (first entry)
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Best Local Similarity 99.5
Matches 379; Conservative
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N-PSDB; ABK48899.
                                                                                                  Human Cyr61 protein
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The present invention describes a method for the prevention or inhibition of breast cancer cell proliferation. The method comprises administration of breast cancer cell proliferation. The method comprises administration of of a compound that inhibits the interaction of a sex steroid receptor with a sex steroid response element of the Cyfel (cysteine rich heparinbinding protein) promoter. Cyfel has cytostatic activity. An antibody (I) which neutralises Cyfel can be used to prevent or inhibit breast cancer cell proliferation by blocking sex steroid induced and growth factor in equivalently of the cyfel DNA, where the growth factor is epidermal, consist in binding epidermal or basic fibroplastic growth factor. (I) can be used to diagnose or stage breast cancer where the level of Cyfel in a costive/suspect breast cancer where the level in normal cost in an increase in the level of Cyfel compared to the level in normal tissue indicates the presence of breast cancer. The level of Cyfel being determined by exposing the tissues to (I), and an increase in the level coff bound antibody by the suspect/postive cell as compared to the normal tissue indicates the presence of breast cancer. The present sequence represents the human Cyfel protein, which is used in the exemplification control of the present invention
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2106; DB 5;
No. 5.6e-161;
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                                                                                                        CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
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The present invention relates to a method for stimulating angiogenesis in a mammal. The method comprises administering a polynucleotide encoding connective tissue growth factor-2 (CTGP-2) or an active fragment or its derivative. The method is useful for stimulating angiogenesis in a mammal preferably human having ischaemia or restenosis or is treated for limb revascularisation which is leg or arm. The invention is useful for inhibiting tumour growth, where anglogenesis is utilised for enhancing the repair of connective and support tissue, promoting the attachment, fixation and stabilisation of tissue implants and enhancing wound healing, hence is useful for treating cardiovascular disease e.g. atherosclerosis, reperfusion injury such as heart failure, angina, atherosclerosis, reperfusion injury such as heart failure, angina, schaered, or regeneration of itssues which is utilised to repair replace or protect tissue damaged by congenital defects, trauma (burns, culcer, etc.), age, disease (e.g. osteoprosis, periodontal disease, liver failure), surgery including cosmetic plastic surgery. The present sailure, surgery including cosmetic plastic surgery. The present
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99.5%; Score 2106; DB 5;
Best Local Similarity 99.5%; Pred. No. 5.6e-161;
Matches 379; Conservative 1; Mismatches 1;
                                                                                                                                         epitope"
                                                                        epitope"
"Immunogenic epitope'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fataccioli V;
                      318. .323
/note= "Immunogenic
337. .343
                                                                                                                                         /note= "Immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calenda V,
                                                                                                                                                                                                                                                                                                                                                     2001WO-US021799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-2001; 2001US-0291642P
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note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD29095.
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                                                                                                                                                                                                                  WO200204480-A2
                                                                                                                                                                                                                                                                                                                                                     11-JUL-2001;
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1 MSSRIARALALVVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of human connective tissue growth factor 2 (CTGF-2), and the polyuncleotide sequence encoding it. The CTGF-2 polypeptide is useful for enhancing the repair of connective and support tissues, for treating skin disorders such as injuries, acne, IV damage or burns, and wrinkled skin, for promoting attachment, fixation and stabilisation of tissue implants, and as an immunogen to produce antibodies. The polyuncleotide sequence encoding CTGF-2 may be used as a hybridisation probe for a cDNA library to isolate the fill-length cDNA and other cDNAs, which have high sequence similarity to the CTGF-2 gene or similar biological activity. The polynucleotides are also useful for identification. The present sequence represents human CTGF-2. Note: The present sequence represents human CTGF-2. Note: The present sequence listing differs from that given in Fig 1 (ABU63223)
                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human connective tissue growth factor 2 polypeptides and polynucleotides useful for enhancing repair of connective and support tissues, and for treating skin disorders, e.g. injuries, acne, UV damage or burns, and wrinkled skin.
                                 301 AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGBTFSKNVMMIQSCKCNYNCP
               AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP
                                                                                                                                                                                                                                                                                                            Human, connective tissue growth factor 2, CTGF-2; support tissue,
tissue repair; skin disorder; injury, acne, UV damage, burn,
wrinkled skin, tissue implant, vulnerary, antiaging, dermatological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
99.5%; Score 2106; DB 6; Length 381;
Best Local Similarity 99.5%; Pred. No. 5.6e-161;
Matches 379; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                Human connective tissue growth factor 2 (CTGF-2) #1.
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                                                                           HANEAAFPFYRLFNDIHKFRD 381
                                                                                             Claim 1; Col 23-24; 20pp; English.
                                                                                                                                                                                    ABU63222 standard; protein; 381
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95US-00459101
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N-PSDB; ACD26170.
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                                                                                                                                                                                                                                                                                                                                                           antiseborrhoeic.
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                  ABU63222;
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                                                                                                                                                                       ABU63222
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities
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                                                                                                                                                                                                                                                                                                          240
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                                           NEDCSKTOPCDHTKGLECNFGASSTALKGICRAOSEGRPCEYNSRIYONGESFOPNCKHO 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidathmatic; antirheumatic; antiarthritic; antivirral; antiinflammatic; antiarthritic; antivirral; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; mannicolicitic controlicitic disorder; antimunomine disorder; antimuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP
NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ
                                                                                                                     CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
                                                                                                                                                                              CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
                                                                                                                                                                                                                                             KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS
                                                                                                                                                                                                                                                                                                KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPLQGGKCIVQTTSWSQCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer associated protein sequence SEQ ID NO:1432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological disease; drug screening
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N-PSDB; AAC78196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WC200055350-A1
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MSSRIARALALVVTLLHITRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL

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antidiabetic; antiaschmatic; antianthritic; antinitaliabetic; antiaschmatic; antialiabetic; antiaschmatic; antialianthritic; antiniflammatory; antithyroid; antiallergic; antibacterial; antiviral; composition neutromobolytic; coagulant; coordicion antiaglogenic. The mootropic; vasotropic; antipaoriatic and antiaglogenic. The mootropic; vasotropic; antipaoriatic and antiaglogenic the polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating to reat disorders of thematopical conditions. Cor inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoical colls, autoimmune disorders, allorgic reactions, grad to result disorders, neurological disease and confidential confidence and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAA942420 represent sequences used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
cytostatic; proliferative; vulnerary; immunomodulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.5%; Score 2106; DB 3; Length 455; 99.5%; Pred. No. 7e-161; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein, comprising CYR61, designated SEC1.
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                                                                                                                                                                                                                                                                                                                                                                                 the present invention
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Matches 379; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 455 AA;
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The invention discloses the isolated human polypeptides, and polymerides encoding them, that have been designated SECX and NOVX. The polymerides can be used for treating, or delaying, the onset of an angiogenic-associated disorder or treating a pathological state in a subject, preferably a mammal. They can also be used in determining the presence of, or predisposition to, a disease associated with altered levels of the polypeptides and polymerications or sequences (SEC1-12), for raising antibodies, for identifying an agent that modulates the expression or activity of the polypeptide, for treating or preventing a NOWX-associated disorder (NOVI-8) and as a pharmaceutical composition comprising the polypeptide, or the antibody. The polypeptides and polymeleotide or the antibody. The polypeptides and polymeleotide or the antibody. The polypeptides and polymeleotides the antibody. The polypeptides are useful in diagnostic applications where their amounts are assessed, or preventing disorders or syndromes such as developmental disorders, immune diseases, signal transduction pathway disorders, metabolic disorders, neurodegenerative disorders (including Alzheimer's disease and parkinson's disease, including obesity), wasting disorders as that of a protores (including Alzheimer's disease and parkinson's disease, cirrhosis, diabetes, infectious disease (bacterial, fungal, protozoal and viral e.g. human immunodeficiency virus, HIV), cancer (e.g. prostate cancer), hypertension, hypotension, multiple cancers, urinary retention, osteoporosis, Crohn's disease, user, for a meniogene te produce antibodise specific for the murching as immunogene to produce antibodise specific for the murching as immunogene to produce antibodise specific for the munical and sease and multiple stations and seasons and such as a such and the seasons and such and seasons and such and such as such and seasons and such as suc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SECX/NOVX polypeptide useful for diagnosing, preventing or treating disorders associated with aberrant expression or activity of SECX/NOVX nucleic acids and proteins e.g., diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhong H;
ta OR, Mysore KK;
'. TaM, Bergh C;
hypertension; hypotension; multiple sclerosis; urinary retention; osteoporosis; Crohn's disease; ulcer; neurological disorder; anxiety; haemophilia; cirrhosis; immunogen; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herrmann JL, Macdougall JR, Zhong H;
Shimkets RA, Gorman L, Craeta OR, Myss
Y, Eisen A, Spaderna SK, Vernet CAM, Be
, Zerhusen BD, Peyman JA, Ellerman K,
JP, Lepley DM, Rieger DK, Burgess CE;
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are the human SEC1-12 and NOV1-8 proteins
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Pred. No. 2.5e-160;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 9; 443pp; English.
                                                                                                                                                                                                                                                           2001US-0261013P.
2001US-0261014P.
2001US-026102BP.
2001US-0261028P.
2001US-0261029P.
2001US-0313170P.
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Best Local Similarity 99.0%;
Matches 377; Conservative
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Boldog F, Shimk
D, Martin GB, Bis
Dipippo VA, Zer
Alsobrook JP, L
                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
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N-PSDB; ABS59522.
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17-AUG-2001;
10-SEP-2001;
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Casman SJ, B
Folkerts O, S
Spytek KA, D
Grosse WM, A
                                                                                          Homo sapiens.
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HASTINGS G
ADAMS M D.
                                                                                                    Sequence 381 AA;
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01-APR-1998;
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                                                        NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCBEWVCDEDSIXDPMEDQDGLLG
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                         MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                             NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSR1YQNGESFQPNCQHO
                                                                                 CTCIDGAVGCIPLCPOELSIPNLGCPNPRLVKVTGOCCEEWVCDEDSIKDPMEDQDGLLG
                                                                                                                     KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLOGOKCIVQTTSWSQCS
                                                                                                                                                          XTCGTGISTRVTNDNPECRLVKETRICBVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY
                                                                                                                                                                      KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY
                                                                                                                                                                                               AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMM1QSCKCNYNCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid molecule, useful for diagnosing or treating prostate
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1, Glatt K, Zhao X,
                                                                                                                                                                                                                                                                                                                                                                              Prostate; cancer; cytostatic; gene therapy; marker.
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, Kamatkar S, Wonsey AM,
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2001US-0314356P.
2001US-0325020P.
2001US-0341746P.
2002US-0362158P.
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25-SEP-2001;
12-DEC-2001;
05-MAR-2002;
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Hoersh S,
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patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequence given in ABB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence was obtained in electronic format directly from WIPO at fit pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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99.1%; Score 2098; DB 7;
Best Local Similarity 99.0%; Pred. No. 2.5e-160;
Matches 377; Conservative 2; Mismatches 2;
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                                                                                                                  The present invention describes human small CCN-like growth factor (SCGF). SCGF has vulnerary and osteopathic activities, and can be used in gene therapy. The SCGF polypeptides and polymucleotides can be used for treating muscle wasting diseases, and polymucleotides can be used for wound healing and tissue regeneration, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CNN family protein which is given in comparison with the human SCGF in the exemplification of the present invention
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                                                                                                                                                                                                                                                                              Gape
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                                                                                                                                                                                                                                                                             ٦,
                                           Novel isolated polynucleotide sequence encoding a human small (growth factor, useful for treating muscle wasting disease, and osteoporosis.
                                                                                                                                                                                                                                                      93.2%; Score 1971.5; DB 5; Length 374; 95.7%; Pred. No. 3.6e-150; ive 2; Mismatches 13; Indels 1;
                                                                                               Disclosure; Fig 2A-D; 33pp; English.
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Matches 358; Conservative
           Adams MD
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                                 WPI; 2002-382150/41
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          Hastings GA,
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AAR90919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ë
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       1. .24 // label= signal_peptide 25. .375
                                                                                                      25. .375
/label= mature_protein
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1A-C; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                           94WO-US007736
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Best Local Similarity 95.7
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI
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N-PSDB; AAT12653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 375 AA;
                                                                                                                                                                                                                                                                                                                                                           12-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                   L2-JUL-1994;
                                                                                                                                                                                                                 WO9601896-A1
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                                                                                                                                                                           Connective tissue growth factor-2; CTGF-2; wound healing; bone disorder; skin disorder; acne; burn; UV damage; stabilisation; tissue implant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotides encoding growth factor polypeptides useful for enhancing the repair of connective tissue and support tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1971.5; DB 2;
Pred. No. 3.6e-150;
2; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                             note= "Cys encoded by ICT"

    .24
    /label= Signal peptide

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                                             AAY31620 standard; protein; 375
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Best Local Similarity 95.7%;
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                             25. .375
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N-PSDB; AAZ11720.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 375 AA;
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                                                                                                                                                                                                                                                                                                           Protein
Misc-difference
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                                                                                                                                              Human CTGF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1995;
                                                                                                                                                                                                                            Homo sapiens
                                                                                                            02-NOV-1999
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                                                                           AAY31620;
                                                                                                                                                                                                                                                                            Peptide
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Gaps

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Indels

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180
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                                                                                                                                                                                                                                                             299
                                                                                                                                                                                                                                                                                  241 SKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPBPVRFT 300
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                                               120
                                                                    61 NEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
                                                                                                                    121 CTCIDGAVG-CIPLCPQELSIPNIGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 179
                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                   300 YAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNC 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; angiogenesis; connective tissue growth factor-2; CTGF-2; tumour; ischaemia; restenosis; tissue repair; wound healing; congenital defect; carditovascular disease; atherosclerosis; heart failure; angina; trauma; burns; osteoporosis; periodontal disease; liver failure; tranquillizer; vulnerary; cosmetic plastic surgery; vasotropic; hepatotropic; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stimulating angiogenesis in a mammal preferably human having ischemia restenosis or is treated for limb revascularization, by administering connective tissue growth factor-2 polypeptide or polynucleotide.
                                                                                                                                                                                                                                                             SKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT
                                                                                                                                                                                                                                                                                                                                                      1 MSSRIVRELALWYTLIHITRVGLSTCPADCHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                              121 CTCIGWRRGACIPLCPQELSLPNLGCPNPRLVKVTGQCCEBWVCDEDSIKDPMEDQDGLL
                                                                                                                                                                                          180 GKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLOGOKCIVOTTSWSOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human alternative connective tissue growth factor-2 (CTGF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fataccioli V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE18108 standard; protein; 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2001; 2001WO-US021799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-2000; 2000US-0217402P, 18-MAY-2001; 2001US-0291642P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC (TRGE ) TRANSGENE SA.
                                                                                                                                                                                                                                                                                                                                                                                                           PHANEAAFPFYRLF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams MD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-2002
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a mammal. The method comprises administering a polynucleotide encoding connective tissue growth factor-2 (CTGF-2) or an active fragment or its connective. The method is useful for stimulating angiogenesis in a mammal preferably human having ischaemia or restenosis or is treated for limb revaccularisation which is leg or arm. The invention is useful for inhibiting tumour growth, where angiogenesis is cutilised for enhancing the repair of connective and support tissue, promoting the attachment, fixation and stabilisation of tissue implants and enhancing wound healing, hence is useful for treating cardiovascular disease e.g. atherosclerosis, reperfusion injury such as heart failure, angina, schemana, and is also used to differentiate, proliferate and attract cells leading to regeneration of tissues which is utilised to repair replace or protect tissue damaged by congenital defects, trauma (burns, close, etc), age, disease (e.g. osteoporosis, periodontal disease, liver failure), surgery including cosmetic plastic surgery. The present
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Sequence 375 AA;

121 CTCIGWRRGACIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 180 61 NEDCSKTOPCDHIKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFOPNCQHQ 120 CTCIDGAVG-CIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 179 GKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQC 239 SKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT 299 241 SKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT 300 YAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNC 359 301 YAGCLSVKKYRPKYCGSCVDGRCCTPQLIRTVKWRFPCEDGETPSKNVMMIQSSKCNYNC 360 61 NEDCRKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFOPNCKHQ 120 1 MSSRIARALALWVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60 1 MSSRIVRELALVVTLLHTTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60 Gaps . Query Match

93.2%; Score 1971.5; DB 5; Length 375;
Best Local Similarity 95.7%; Pred. No. 3.6e-150;
Matches 358; Conservative 2; Mismatches 13; Indels 1; PHANEAAFPFYRLF 373 PHANEAAFPFYRLF 374 180 360 121 240 300 g ò 셤 ò g ₹ 셤 δ 셤 ò g ò

Search completed: April 22, 2004, 17:56:33 Job time : 51.1316 secs

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1 MSSRIARALALVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09142569
Patent No. 6413735
GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                    Sequence
Sequence
Sequence
Sequence
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OTHER INFORMATIÖN: "Human Cyr61 amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
CONTRY: United States of America
CONTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPES FLORY disk
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-APPL-1999
CLASSIFICATION NUMBER: US/09/142,569
FILING DATE: 02-APPL-1999
ATTORNEY/AGENT INFORMATION:
NAME: Cloudy Day:
NAME: Cloudy DAY:
TELEFRATION NUMBER: 36.107
TELEFRATION NUMBER: 36.107
TELEFRATION NUMBER: 36.107
TELEFRATION NUMBER: 36.107
TELEFRATION NUMBER: 312/474-6300
TELEFRAX: 312/474-6300
TELEFRAX: 312/474-6300
TELEFRAX: 312/474-6300
TELEFRAX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERESTICS:
               US-08-468-847B-14
US-08-468-847B-16
US-08-468-847B-16
US-09-182-145-4
US-09-182-145-7
US-09-182-145-7
US-09-182-145-7
US-09-182-145-5
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  FEATURE
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1 MSSRIARALALVVTLHLTR......ANEAAFPFYRLFNDIHKFRD 381
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Compugen Ltd.
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US-08-468-815-2
US-08-468-8478-11
US-08-468-8478-11
US-09-142-569-2
US-09-142-569-3
US-09-142-569-3
US-09-142-569-6
US-09-054-368-2
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Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/POCKET NUMBER: 3258
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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US-08-468-847B-12
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TOPOLOGY: L
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                                                                                                                            301 AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP 360
1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
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                                                                                                       CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVXVTGQCCEEWVCDEDSIKDPMEDQDGLLG
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ADAMS, MARK D
TILLE OF INVALION: CONNECTIVE TISSUE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: 9410 KBY WEST AVENUE
CITY: ROCKVILLE
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NAME: JONGTHAN L. KLEIN
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PP126P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8604
TELEFFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,815
FILING DATE: 08-U1-1999
CLASSIFICATION: <UNKNOWN>
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Patent No. 6534630
GENERAL INFORMATION:
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LENGTH: 381 amino acids
TYPE: amino acid
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Best Local Similarity 99.5%
Matches 379; Conservative
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                                                                                                                                61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAOSEGRPCEYNSRIYONGESFOPNCKHO 120
                                                                                                                                                                                                   121 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180
1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKOL 60
                                                                                                                                                                                                                                              121 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
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Patent No. 2780263
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STREET: 6 CCUNTY: USA
COUNTY: USA
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 13M FS/2
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,847
FILING DATE: 6 June 1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
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241 SKTCGTGISTRVTNDNPECRLVKETRICGVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFT 300
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                                                                                              Length 375;
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Patent No. 5780263
GENERAL INFORMATION:
APPLICANT: Heather Greeg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESSE:
ADDRESSEE: CRCCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                              Score 1964.5; DB 2
Pred. No. 1.3e-163;
2; Mismatches 14;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M P8/2
COMPUTER: 18M P8/2
COMPUTER: 18M P8/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,847B
FILING DATE: 6 June 1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFRENCE/POCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1704
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                  Query Match
Best Local Similarity 95.5%;
Matches 357; Conservative
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; MOLECULE TYPE: PROTEIN US-08-459-101A-2
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                                                                                              1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
                                                                                                                                    1 MSSRIVRELALVVTLLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGCGCCKVCAKOL 60
                                        1; Gaps
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Patent No. 5545300

GENERAL INFORMATION:
TITLE OF INVENTION: Connective Tissue Growth Factor-2
INTLE OF INVENTION: Connective Tissue Growth Factor-2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYPNE, BAIN, GILFILLAN,
ADDRESSEE: CARELLA, BYPNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
Best Local Similarity 95.7%; Pred. No. 3.3e-164;
Matches 358; Conservative 2; Mismatches 13; Indels
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 12 S. SOFTWARE:
COMPUTER: 12 SOFTWARE: 13 SOFTWARE: 12 SOFTWARE: 13 SOFTWARE: 12 SOFTWARE: 13 SOFTWARE: 12 SOFTWARE: 13 SOF
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TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201-994-1744
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61 NEDCSKTÓPCDHTKGLECNFGASSTALKGICRAQSEGRPCEÝNSKIÝQNGESFQPNCKHQ 120
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                                                                                                                                                NAME/KEY: misc feature OTHER INFORMATION: "Mouse Cyr61 amino acid sequence" SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                  Length 379;
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APPLICANT: Hastings, Gregg A. and Adams, Mark D. TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CECCHI, STEWART & OLSTEIN
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STRET: 6 BECKER FARM ROAD
STRET: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                               Query Match
91.2%; Score 1929; DB 4;
Best Local Similarity 90.9%; Pred. No. 1.7e-160;
Matches 348; Conservative 10; Mismatches 19;
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APPLICATION NUMBER: US/08/468,847B
FILING DATE: 0 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                              LENGTH: 379 amino acids TYPE: amino acid
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SOFTWARE: WORD PERFECT 5.1
          SEQUENCE CHARACTERISTICS
                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH
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                                                                                                                              FEATURE
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TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
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ADDRESSEE: Marshall, O'Toole, Geretein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                            9
                                                                                                                                                                         Length 379;
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STATE: Illinois
CONTRY: United States of America
ZIP: 60606-640
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRING APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAWE: Clough, David W
REGISTRATION NUMBER: 36,107
REPRENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                            19;
                                                                                                                                                                         Query Match
Best Local Similarity 90.9%; Pred. No. 1.7e-160;
Matches 348; Conservative 10; Mismatches 19;
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Patent No. 6413735
GENERAL INFORMATION:
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; LENGTH: 379 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-468-847B-11
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INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: PIBROGEN, INC
APPLICANT: SCHUTCH Brian
APPLICANT: SCHUTCH ARGAGATE
APPLICANT: ALLEN, MARGAGATE
APPLICANT: ALLEN, MARGAGATE
APPLICANT: ALLEN, MARGAGATE
APPLICANT: CARNICHAEL, David
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
FILE REPERENCE: FIBROLIOO-1
CURRENT APPLICATION NUMBER: US/09/292,036
FRIOR APPLICATION NUMBER: US 09/187,478
FRIOR APPLICATION NUMBER: US 09/187,478
FRIOR PILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.0
SSQ ID NO 3
EENGTH: 348
                                                                                                                                                                                                                                                                 61 QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCPAK-DGAPCVFGGSVYRSGESFQSSCK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 IGKELGFDASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 FELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVBFKCPDGEIMKKNNMFIKTCACHY 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 ACSKTCGMGISTRVTNDNTFCRLEKQSRLCMVRPCBADLEENIKKGKKCIRTPKIAKPVK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOLNEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117
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                                                                                                                                                                                                                                                                                                                                                                  119 HQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGL
                                                                                  1 MSSRIARALALWVTLLHLTRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCAK
                                                                                                                                             1 MLASVAGPVSLALVLLLCTRPATGQDCSAQCQCAREAAPRCPAGVSLVLDGCGCCRVCAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KDRTVVGPALAAYRLEDTFGPDPTMM-----RANCLVQTTEWS
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           Gaps
              40;
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              58; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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46.6%; Pred. No. 2.7e-75;
iive 57; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 NCPGDNDIFESLYYRKMYGDM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCPHANEAAFPFY--RLFNDI 376
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Patent No. 6358741
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Best Local Similarity 46.6
Matches 178; Conservative
              176; Conservative
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GENERAL INFORMATION:
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-292-036-3
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                  Matches
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patent No. 656268

Sequence 2, Application US/09582337

patent No. 656268

GENERAL INPORMATION:

TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor

TITLE OF INVENTION: and Medicinal Uses Thereof

TITLE OF INVENTION: and Medicinal Uses Thereof

FILE REFERENCE: J1-009PCT

CURRENT APPLICATION NUMBER: US/09/582,337

CURRENT FILING DATE: 1997-12-25

PRIOR FILING DATE: 1997-12-25

PRIOR FILING DATE: 1998-12-15

SOFTWARE: PRIOR FILING DATE: 1998-12-15

SOFTWARE: PATENT OF USE: 1208-12-15

SOFTWARE: PATENT OF USE: 1208-12-15

SEQ ID NO: 27

LENGTH: 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 LNEDCSRIQPCDHTKGLECNFGASPAATNGICRAQSEGRPCEYNSKIYQNGESFQPNCKH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 QCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 GKELGFDASEVELTRNNELIAVGKGRSLKRLFVFGMEP--RILYNPLQGQKCIVQTTSWS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 SKEFGLDASEGELTRNNELIAIVKG-GLKMLPVFGSEPQSRAFENP----KCIVQTTSWS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

80.1%; Score 1695; DB 1;
Best Local Similarity 81.0%; Pred. No. 4.5e-140;
Matches 311; Conservative 20; Mismatches 41;
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Pred. No. 2.5e-75;
                                            33,073
ER: 325800-442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 NCPHANEAAFPFYRLFNDIHKFRD 381
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3256
TELECOMMUNICATION INPORMATION:
TELEPHONE: 201-994-1700
INPORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 375 AMINO ACIDS
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                                                                                                                                                                                                                                                                                           1: 375 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
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Best Local Similarity
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CRGANISM: Rat
US-09-582-337-2
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US-08-468-847B-13
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                                 206 SACSKTCGMGISTRVTNDNTFCRLEKQSRLCMVRPCBADLBENIKKGKKCIRTPKIAKPV
                                                                                              178 LLGKELGFDASEVELTRNNELLAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSW
                                                                                                                                                                                            237 SQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09142569
Patent No. 6413735
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
ADDRESSEE: MATCHAIL, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
CONTRY: United States of America
COUNTRY: United States of America
CONTRY: United States of America
ZIP: 6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NAMER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: Chiknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cloud, David W.
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 28,107
TELEFAN: 312/474-6300
TELEFAN: 312/474-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: "Figp12 amino acid sequence" SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                    357 YNCPHANEAAFPFY -- RLFNDI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                 326 YNCPGDNDIFESLYYRKMYGDM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity
Matches 177; Conservat
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US-09-142-569-6
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                                                                                                                                                                                                 297 RFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCN 356
          178 LLGKELGFDASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSW 236
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                                                  ---KDRTAVGPALAAYRLEDTFGPDPTMM-----RANCLVQTTEW
                                                                                                     SOCSKICGIGISTRVINDNPECRLVKETRICEVRPCGOPVYSSLKKGKKCSKTKKSPEPV
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APPLICANT: Hastings, Gregg A. and Adams, Mark D.
APPLICANT: Hastings, Gregg A. and Adams, Mark D.
TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
STREET: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 44.8%; Score 948.5; DB 1;
Best Local Similarity 46.3%; Pred. No. 6.1e-75;
Matches 177; Conservative 58; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
CURRENT APPLICATION DATA:
FILING DATE: 6 June 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                            357 YNCPHANEAAFPFY -- RLFNDI 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGIGSTRATION NUMBER: 33.073
REFRENCE/DOCKET NUMBER: 32581
TELERIOMUNICATION INFORMATION:
TELERIOMICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 348 AMINO ACIDS
TYPE: AMINO ACID
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Patent No. 5408040
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bracham Jr., Douglas M.,
TITLE OF INVENTION:
UNDER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 NCPHANEAAFP--FYR-LFNDI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 NCPGDND-IFPCMYYRKMYGDM 346
                326 NCPGDND-IFPCMYYRKMYGDM 346
NCPHANEAAFP--FYR-LFNDI 376
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.3
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Rat
US-09-292-036-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-167-628-2
                                                                  RESULT 13
US-09-292-036-2
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                                                                                                                       236
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                                                                                                                                                                              SOCSKICGIGISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV 296
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              KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC 117
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                             HOCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGL
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                                                                                                                       178 LLGKELGFDASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.8%; Score 948; DB 4; Length 347
46.3%; Pred. No. 6.8e-75;
ive 58; Mismatches 105; Indels
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Patent No. 634829;
GENERAL INFORMATION:
APPLICANT: Schmidth.
TITLE OF INVENTION: Connective Tissue Growth (CTV:
TITLE REFERENCE: 08766/004001
CURRENT APLICATION WUMBER: US/09/187,478
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT;
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast
US-09-187-478-2
                                                                                                                                                                                                                                                                                         YNCPHANEAAFPFY--RLFNDI 376
                                                                                                                                                                                                                                                                                                                  YNCPGDNDIFESLYYRKMYGDM 347
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Matches 177; Conservative
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US-09-187-478-2
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Best Local &
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Sequence 2, Application US/09292036

Patent No. 635841

GENERAL INFORMATION:
APPLICANT: FIEROGEN, INC
APPLICANT: ALLEN, Margaret
APPLICANT: ALLEN, Margaret
APPLICANT: ALLEN, Margaret
APPLICANT: APPLICANT: OCNNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
TITLE OF INVENTION: CONNECTIVE 1999-04-14
TITLE OF INVENTION NUMBER: US 09/292,036
CURRENT FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-04-14
SPRIOR FILING DATE: 1999-04-14
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARTIEN FG-Bese #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,680
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
  Bradham Jr., Douglas M.,
FENTION: CONNECTIVE TISSUE GROWTH FACTOR
                                                              ADDRESSEE: Spensley Horn Jubas & Lubitz STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILLING DAIL:
ATTORNEY AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REPERENCE/DOCKET NUMBER: PD-1294
TELEPHONE: 619-455-5110
TELEFAX: 619-455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: APPLICATION NUMBER: US/07/752,427 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 349 amino acids
amino acid
APPLICANT: Bradham Jr.,
TITLE OF INVENTION: CONN
NUMBER OF SEQUENCES: 2
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Spensley HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                       STATE: C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 GISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLS 305
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                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph. D., John W.
REGISTRATION NUMBER: 31,678
TELECOMMUNICATION: 1000 NOCKET NUMBER: PD-1294
TELEPHONE: 619-455-5100
                   ADDRESSEE: Spensley Horn Jubas STREET: 4225 Executive Square, CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 349 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-167-628-2
      CORRESPONDENCE ADDRESS:
                                                              CITY: La Jo
STATE: CA
COUNTRY: US
ZIP: 92037
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173 -----TVVGPALAAYRLEDTFGPDPTMI-----RANCLVQTTEWSACSKTCGM 215
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                                                                                                                           9 LALVVTLIHLTRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCAKQLNEDCSK
                                                                                                                                                                                                                                                                                                                      187 ASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGT
     Length 349;
                                                   58; Mismatches 101; Indels
44.8%; Score 947; DB 1; ilarity 46.6%; Pred. No. 8.3e-75; Conservative 58; Mismatches 101
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  Query Match
Best Local Similarity
Matches 174; Conserv
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%30-08-386-680-2 ; Sequence 2, Application US/08386680 ; Patent No. 5585270 ; GENERAL INPORMATION:

Grotendorst, Gary

APPLICANT:

Job time : 17.5434 secs

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Sequence 4, Application US/10053753
Publication No. US20020150986A1
GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATCHAIL, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COUNTRY: United States of America
ZIP: 6606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,753
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET VUMBER: 36,107
REFERENCE/DOCKET VUMBER: 36,107
TELEPHONE: 312/474-6448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
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US-10-053-753-4
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                                                                                                             April 22, 2004, 17:58:40; Search time 38.6013 Seconds (without alignments) 2728.846 Million cell updates/sec
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Sequence 2, App
Sequence 2, App
Sequence 42, A
Sequence 42, A
Sequence 42, A
Sequence 61, A
Sequence 1432,
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2116
1 MSSRIARALALVVTLLHLTR......ANBAAFPFYRLFNDIHKFRD 381
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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i US-10-182-432-4

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i US-10-394-015-5

i US-10-381-644-2

i US-10-381-644-2

i US-10-99-322-43

i US-10-99-322-43

i US-10-044-564-44

i US-10-044-564-44

i US-10-044-564-44
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                                                                                                                                                                                                                                                                                                                                1133595 seqs, 276475211 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                  Copyright
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Match
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                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                            Scoring table:
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Maximum DB (
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No.
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US-10-099-322-2	10-099-3	-10-044-564	10-044-5	153-625B	901-9	153-625B-	053-7	099-322-	182-432	044-564-4	464-368-6	464-368-6	153-625B	464-368-6	245-977-	464-368-	US-10-390-986-2		53-625B-	10-053-753	10-245-977-	10-182-432-	-464-368-	10-080-173-	10-101-040	10-101-040-	10-011-859-	10-053	US-10-060-036-173	
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ALIGNMENTS

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240
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                                                                                                                                                                                                         101 AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP
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                             301 AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCP
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  KELGFDASEVELTRINNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS
                                                                                         241 KTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSSRIARALALVVTLIHITRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Adams, Mark

APPLICANT: Adams, Mark

APPLICANT: Calenda Valetie

TITLE OF INVENTION: Connective Tissue Growth Factor-2

TITLE OF INVENTION: Connective Tissue Growth Factor-2

CURRENT APPLICATION NUMBER: US/09/901,910

CURRENT FILING DATE: 2001-07-11

PRIOR PILING DATE: 1999-00-08

PRIOR APPLICATION NUMBER: 09/489,101

PRIOR PILING DATE: 1995-06-02

PRIOR APPLICATION NUMBER: 60/217,402

PRIOR PILING DATE: 1994-07-12

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2001-05-18

SOFTWARE: PLENTING DATE: 2001-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2106; DB 10;
Pred. No. 1.7e-171;
1; Mismatches 1;
                                                                                                                                                                                                                                                                               361 HANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                                                                                                                                                                                     361 HANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09901910 Publication No. US20030012768A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.5%;
Matches 379; Conservative 1
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ORGANISM: homo sapiens
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Publication No. US20040002124A1
GENERAL INFORMATION:
TITLE OF INVENTION: CXR61 COMPOSITIONS AND METHODS
FILE REFERENCE: 214448/00029
CURRENT APPLICATION NUMBER: US/10/182,432
CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 38
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                   NAME/KEY: misc feature
OTHER INFORMATION: "Human Cyr61 amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                      100.0%; Score 2116; DB 13;
100.0%; Pred. No. 2.4e-172;
iive 0; Mismatches 0;
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Matches 381; Conservative
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  FEATURE
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CURRENT APPLICATION NUMBER: US/10/394,015
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FILING DATE: 2001-01-11
APPLICATION NUMBER: 60/313,170
FILING DATE: 2001-08-17
APPLICATION NUMBER: 10/044,564
FILING DATE: 2002-01-11
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's Sequence 42, Application US/10099322
'publication No US20030215449A1
'GENERAL INFORMATION'
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Best Local Similarity 99.5
Matches 379; Conservative
                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-015-5
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TILLE OF INVENTION: Connective Tissue Growth Factor-2
FILE REFERENCE: PP126P102
CURRENT APPLICATION WINBER: US/10/294,796
CURRENT FILING DATE: 2002-11-15
PRIOR PPLICATION NUMBER: US 09/348,815
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR PILING DATE: 1999-07-12
NUMBER OF SEQ 1D NOS: 6
SOFTWARE: PatentIn version 3.1
LENGTH: 381
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Publication No. US20030180891A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Connective Tissue Growth Factor-4
FILE REFERENCE: PF467
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Pred. No. 1.7e-171;
1; Mismatches 1;
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                                   361 HANEAAFPFYRLFNDIHKFRD 381
                                                             ; Sequence 2, Application US/10294796; Publication No. US20030078391A1; GENERAL INFORMATION:
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Best Local Similarity 99.5%;
Matches 379; Conservative
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CRGANISM: Homo sapiens
US-10-294-796-2
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US-10-294-796-2
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CURRENT FILING DATE: 2003-03-24

FRICA PAPLICATION NUMBER: US/09/325,019

PRIOR FILING DATE: 1999-06-03

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/088,320

PRIOR RILING DATE: EARLIER FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATCHIN VEr. 2.0

SEQ ID NO 5
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CURRENT FILING DATE: 2002-09-11

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,026

PRIOR PILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,026

PRIOR APPLICATION NUMBER: 60/261,029

PRIOR PILING DATE: 2001-01-11

PRIOR PILING DATE: 2001-01-11
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Pred. No. 1.7e-171;
1; Mismatches 1;
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Gaps

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121 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180
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        Length 381;
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APPLICANT: American Home Products Corporation
APPLICANT: Sampath, Deepak
APPLICANT: Sampath, Deepak
APPLICANT: Sampath, Deepak
APPLICANT: Suppath, Pining
APPLICANT: Minnskar, Richard
ITILE OF INVENTION: Use of Cyr61 in the treatment and
ITILE OF INVENTION: Use of Cyr61 in the treatment and
ITILE APPLICANT: NUMBER: US/10/381,644
CURRENT APPLICATION NUMBER: US/10/381,644
CURRENT APPLICATION NUMBER: 06/236,887
PRIOR PILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
WUMBER: OF SEQ ID NOS: 3
SOFTWARE: FRAESEQ for Windows Version 3.0
SED ID NO 2.
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     Score 2106; DB 15;
Pred. No. 1.7e-171;
1; Mismatches 1;
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        Query Match
Best Local Similarity 99.5%;
Matches 379; Conservative
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ORGANISM: Homo Sapien
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Sequence 42, Application US/10044564

Publication No. US2040018196A1

GENERAL INFORMATION:

APPLICANT: Mezes et al.

ITILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILER REFERENCE: 21402-240

CURRENT APPLICATION NUMBER: US/10/044,564

CURRENT APPLICATION NUMBER: 00/261,014

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,013

PRIOR PELING DATE: 2001-01-11

PRIOR PELING DATE: 2001-01-11
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; NUMBER OF SEQ ID NOS; 324; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 42; LENGTH: 381; TYPE: PRT; CANNISM: HOMO SAPIENB US-10-099-322-42
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                                                                                                                                                                                                                                                                                    Sequence 61, Application US/10464368
Publication No. US20040023356A1
GENERAL INFORMATION
APPLICANT: Krumlauf, Robb
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REPRENCE: 40716-1P-017
CURRENT PELICATION NUMBER: US/10/464,368
PRIOR PPLICATION NUMBER: 60/388,970
PRIOR FILING DATE: 2003-06-14
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PATENTIN UVERSION 3.2
SEQ ID NOS: 140
SEQ ID NOS: 140
SEQ ID NOS: 140
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99.5%; Score 2106; DB 16; Length 381;
Best Local Similarity 99.5%; Pred. No. 1.7e-171;
Matches 379; Conservative 1; Mismatches 1; Indels 0
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ORGANISM: HOMO SAPIENS
US-10-464-368-61
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US-10-464-368-61
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Publication No. US20030215449A1

GENERAL INFORMATION:

TILLS OF INVENTION:

TILLS OF INVENTION:

CURRENT APPLICATION WUMBER: US/10/099,322

CURRENT APPLICATION NUMBER: 06/261,014

PRIOR PILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,014

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR APPLICATION NUMBER: 60/261,013

PRIOR APPLICATION NUMBER: 60/261,013

PRIOR APPLICATION NUMBER: 60/261,013

PRIOR APPLICATION NUMBER: 60/261,013

PRIOR APPLICATION NUMBER: 60/261,013
Sequence 1432, Application US/09925301

Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acide, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFFWARR: Patentin Ver. 2.0

SEQ ID NO 1432

LENGTH: 455
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Pred. No. 2.1e-171;
1; Mismatches 1;
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Best Local Similarity 99.5%;
Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-09-925-301-1432
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE REFERENCE: 21402-2402.099,322
CURRENT APPLICATION NUMBER: US/10/099,322
CURRENT FILING DATE: 2000-09-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2002-01-11
PRIOR PILING DATE: 2003-01-11
                                                                                                                                                                                           Length 381;
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                                                                                                                                                                                           Query Match 99.4%; Score 2103; DB 15; Best Local Similarity 99.2%; Pred. No. 3.1e-171; Matches 378; Conservative 2; Mismatches 1;
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Publication No. US20030215449A1
GENERAL INFORMATION:
           SOFTWARE: Patentin Ver. 2.1
                               ; SEQ ID NO 43
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-564-43
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Sequence 43, Application US/10044564
Publication No. US20040019196A1
GENERAL INFORMATION:
APPLICANT: Mezes et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-240
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CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/261,014
PRIOR APPLICATION NUMBER: 60/261,014
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR PLING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR PLING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR PLING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR PLING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SEQ ID NO 43
LENGTH: 381
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Bochegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Gendege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Monsey, Angela M.
APPLICANT: Monsey, Angela M.
APPLICANT: Anderson, Dustin
APPLICANT: Maderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: MAGERSON, Dustin
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APPLICANT: MAGERSON, Dustin
APPLICANT: MAGERSON, Dustin
APPLICANTON WUMBER: US/10/205, 823
CURRENT APPLICATION NUMBER: 06/314, 356
PRIOR FILING DATE: 2001-08-25
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-25
PRIOR FILING DATE: 2001-08-26
PRIOR FILING DATE: 2001-08-25
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR PR
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   NEDCSKTOPCDHTKGLECNFGASSTALKGICRAOSEGRPCEYNSRIYONGESFOPNCOHO 120
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                                               61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFQPNCKHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-205-823-84
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REPERNOE: 21402-240
FULR PERERNOE: 21402-240
CURRENT APPLICATION NUMBER: US/10/044,564
CURRENT FILING DATE: 2002-05-09
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR PELING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR FILING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
PRIOR PELING DATE: 2001-01-11
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Pred. No. 5.5e-171;
1; Mismatches 2;
99.2%; Score 2100; DB 15;
llarity 99.2%; Pred. No. 5.5e-171;
Conservative 1; Mismatches 2;
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US-10-044-564-44
Sequence 44, Application US/10044564
Publication No. US20040018196Al
GENERAL INFORMATION:
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Best Local Similarity 99.2%;
Matches 378; Conservative
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Matches 378, Conserv
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361 HANEAAFPFYRLFNDIHKFRD 381
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Search completed: April 22, 2004, 18:08:17 Job time : 39.6013 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run. on:

April 22, 2004, 17:53:39 ; Search time 16:5434 Seconds (without alignments) 2215.320 Million cell updates/sec

US-09-495-448A-4 2116 1 MSSRIARALALVVTLIHLTR......ANEAAFPFYRLFNDIHKFRD 381 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ਲ	10 prot	beta IG-M2 protein	nective	NOV protein - chic	gene novH protein	hypothetical prote	hypothetical prote	Balbiani ring 3 pr	MEGF6 protein - ra	zonadhesin - mouse	pr	mucin-like peptide	laminin B1k chain	notch4 - mouse	hypothetical prote	protein F40B10.4 [mucin, submaxillar	mucin 5AC (clone L	mucin 2 precursor,	ed 1	mucin - rat	tenascin-X - bovin	hypothetical prote	e pr	protein	n MUCSB, tr	а.	<u>م</u>
SUMMARIES	ID	A35669	A41428	057	A40551	S20078	138069	T26972	T27283	S08167	T13954	T42215	A39804	A42112	A53612	T09059	T22025	D89711	T03099	A57534	A43932	T42626	m	262		261	442	vo	A36665	ω
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	Query Match Length	379	375	348	349	351	357	1111	1620	1700	1574	5376	1178	837	1170	1964	601	601	13288	1042	3020	1025	1034	4135	1101	2437	2703	1056	1480	2531
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56985	A40558	T25169	T09070	AGRT	S53868	T23433	T37316	AGCH	VWHU	A40043	A55035	B36665	T42218	T23064	F87908
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1168 2	1170 2													6.2 2823	
6.4 1168 2	1170 2	6.4	6.4	6.3		6.3	6.3	6.3	. 9	6.3	6.2	6.2	6.2		6.2

ALIGNMENTS

RESULT 1 A35669 Gene CYR61 protein precursor - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Jacesaion: A3569; Massaion 18-Nov-1992 #text_change 05-Nov-1999 C.Jacesaion: A3569; Mal319; Sid446 Mol. Cell. Biol. 10, 3368-3577, 1990 A.Fitle: Expression of cyr61, a growth factor-inducible immediate-early gene. A.Reference number: A35669; MUID:90287146; PMID:2355916 A.Status: preliminary A.Status: preliminary A.Beraicher Type: mRNA A.Beraicher 279 - A379 - CARA	A;Cross-references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206 A;Cross-references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206 A;Note: the authors translated the codon GAT for residue 337 as Gln R;Latinkic, B.V.; O'Brien, T.P.; Lau, L.F. Nucleic Acids Res. 19, 3261-3367, 1991 A;Title: Promoter function and structure of the growth factor-inducible immediate early A;Reference number: 148319; MUID:91288203; PMID:2062642 A;Accession: I48319 A;Status: translated from GB/BMBL/DDBJ A;Accession: Laps DNA A;Molecule type: DNA A;Residues: 1-379 cRES> A;Cross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g50633 A;Cross-references: EmBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g50633 A;Note: the authors did not translated the codon for residue 108 A;Note: the authors translated the codon GAT for residue 337 as Gln	C;Genetics: A;Gene: C1213; 93/1; 208/1; 279/3 A;Introns: 21/3; 93/1; 208/1; 279/3 C;Superfamily; von Willebrand factor type C repeat homology C;Superfamily: von Willebrand factor type C repeat homology Cuty Match Ouery Watch Best Local Similarity 90.9%; Pred. No. 1:3-134; Matches 348; Conservative 10; Mismatches 19; Indels 6; Gaps 2;	1 MSSRIARALALVYTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60 	61 NEDCSKTQPCDHTKGLECNFGASSTALKGICEAQSEGRPCEYNSRIYQNGESFQPNCQHQ 120	121 CTCIDGAVGCIFLCPQELSLPNIGCPNPRLVKVTGQCCEEWVCDBDSIKDPMEDQDGLLG 180 	181 KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQ 238
RESULT 1 A3569 Gene CYR61 protein Gspecies: Mus musc C; Date: 28-Sep-1990 C; Accession: A35669 R; O'Brien, T.P.: Ya Mol. Cell. Biol. 10 A; Title: Expression A; Accession: A35669 A; Status: prelimina A; Molecule type: mR A; Molecule type: mR A; Molecule type: mR A; Molecule type: mR	A.Cross-references A,Note: the authors R.Latinkio, B.V.; O Nucleic Acids Res. A,Title: Promoter f. A,Reference number: A,Rocession: 140319 A,Residues: translate A,Residues: 1379 c. A,Cross-references: A,Note: the authors A,Note: the authors	C;Genetics: A;Gene: CYSE1 A;Introns: 21, C;Superfamily F;99-166/Doma: Ouery Match Best Local Matches 341,	& g	දු දු	% q	oy da

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Length 348;
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A;Status: preliminary
A;Molecule type: mRNA
A;Roesidues: 1-349 <-08m>
A;Cross-references: EMBL:X78947; NID:g474933; PID:g474934
                                                                                                                                                                                                                                                                                               45.0%; Score 952.5; DB 2;
46.6%; Pred. No. 7.9e-63;
iive 57; Mismatches 106;
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Matches 178; Conservative
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beta IG-M2 protein precursor - mouse
cispecies Mus musculus (house mouse)
cjopecies Mus musculus (house mouse)
cjopecies Mus musculus (house mouse)
cjopecies 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 01-Dec-2000
cjocession: A40578; A53228
Ribrunner, A.; Olinn, J.; Neubauer, M.; Purchio, A.F.
DNA Cell Biol. 10, 293-300, 1991
AjTile: Identification of a gene family regulated by transforming growth factor-beta.
A;Reference number: A40578; MUID:91229699; PMID:2029337
                                                                                                                                                                                                                                      RESULT 2
A41428
CEF-10 protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Decies: Gallus gallus (chicken)
C;Decies: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jul-2000
C;Accession: A41428
R;Simmons, D.L; Levy, D.B.; Yannoni, Y.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
A;Title: Identification of a phorbol ester-repressible v-src-inducible gene. A;Reference number: A41428 MUID:89145206; PMID:2537491
A;Accession: A41428
A;Accession: A41428
A;Accession: A41428
A;Accession: A41428
A;Accession: A41428
A;Cross-references: GB:J04496; NID:G211435; PIDN:AAA48661.1; PID:G211436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                             TYAGCSSVKYYPPKYCGSCVDGRCCTPLQTRTVKMFFCEDGEMFSKNVMIQSCKCNYN 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 QCTCIDGAVGCIPLCPQELSLPNLGCPSPRLVKVPGQCCEEWVCDES--KDALBELEGFF 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 QCSKTCGTGISTRVINDNPDCKLIKETRICEVRPCGQP8YASLKKGKKCTKTKKKSPSPVR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTYAGCSSVKKYRPKYCGSCVDGRCCTPQQTRTVKIRFRCDDGETFTKSVMMIQSCRCNY 352
                                       CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296
                                                                           TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN 358
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     CSKTCGTG1STRVTNDNPECRLVKETR1CEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
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                                                                                                                                                                        CPHPNEASFRLYSLFNDIHKFRD 379
                                                                                                                                                  CPHANEAAFPFYRLFNDIHKFRD 381
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A; Residues: 1-349 <BRA>
A; Cross-references: 0B:M92934; GB:M36965; GB:S56201; NID:g180923; PIDN:AAA91279.1;
R; Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
B:Dahitted to the EMBL Data Library, April 1994
A; Description: Differential cloning and expression of human connective tissue growt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 KFELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNMMFIKTCACH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 QHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   connective tissue growth factor - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C;Accession: A40551; 844205
R;Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A;Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by A;Reference numbor: A40551; MUD:91373462; PMID:1654338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 LLGKELGFDASBVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 SQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSSRIARALALVVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
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PID:9201946
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expression in Wilms tu
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G;Species: Homo sapiens (man)
G;Species: Homo sapiens (man)
G;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 05-Nov-1999
C;Accession: 138069
R;Martinerie, C; Huff, V; Joubert, I; Badzioch, M; Saunders, G; Strong, L;
Oncogene 9, 2720-2732, 1994
A;Title: Structural analysis of the human nov proto-oncogene and expression in N
A;Reference number: 138069; MulD:94436229; PMID:7520150
A;Reterence number: 138069; MulD:94436229; PMID:7520150
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-357 <RES>
A;Cross-references: EMBL:X78351; NID:9587422; PIDN:CAA55146.1; PID:9825696
C;Genetics:
A;Gene: novH
A;Introns: 28/3; 104/1; 188/1; 259/3
A;Introns: 28/3; 104/1; 188/1; 259/3
C;Superfamily: thrombospondin type 1 repeat homology <THRI>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T26972
R;Harris, B.
295 PVRFIYAGCLSVKKYRPKYCGSCVDGRCCIPQLIRIVKARFRCEDGEIFSKNVAMIQSCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 CGMGFSTRVTNRNRQCEMLKQTRLCMVRPCEQEPEQPTDKKGKKCLRTKKSLKAIHLQFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 GCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKWRFRCEDGETFSKNVMMIQSCKCNYNCPH
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Best Local Similarity 43.1%; Pred. No. 1.3e-53;
Matches 157; Conservative 48; Mismatches 120;
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327 CHGNCPQSNNAFF 339
                                                                                                                                           CNYNCPHANEAAF 367
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30.078
NOV protein - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: S20078
R;Joliot, V.; Martinerie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, J.; Perk
M,71:Le: Proviral rearrangements and overexpression of a new cellular gene (nov) in myell A;Reference number: S20078
M,71:Le: Proviral rearrangements and overexpression of a new cellular gene (nov) in myell A;Residus: preliminary
A;Molecule type: mRNA
A;Residues: preliminary
A;Residues: 1-351 <JOL>
A;Cross-references: EMBL:XS9284; NID:g63702; PIDN:CAA41975.1; PID:g63703
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                                                                                                                                                                                                                                                           AVGCIPICPOBLSLPNLGCPNPRLVKVTGQCCEBWVCDBDSIKDPMEDQDGLLGKELGFD 186
                                                                                                                                                                                                                                                                                                                                                                            -----TVVGPALAAYRLEDTFGPDFTMI-----RANCLVQTTEWSACSKTCGM 215
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                                                                                                                        9 LALVVTLLHLTRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCAKQLNEDCSK
                                                                                                                                                                                                                                                                                                                                      187 ASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIVITLIHLTRLALS - - - - TCPAAC - - HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDC
                                                                Gaps
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                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 351;
                           Length 349;
                      tch 44.8%; Score 947; DB 2; Length 34: al Similarity 46.6%; Pred. No. 2e-62; 174; Conservative 58; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.2%; Score 851.5; DB 2;
Best Local Similarity 44.0%; Pred. No. 2.1e-55;
Matches 164; Conservative 44; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FESLYYRKMYGDM 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFPFY--RLFNDI 376
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                        Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                              173
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                                                              Matches
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Dalbian ring 3 protein - midge (Chironomus tentans)
C;Species: Chironomus tentans
C;Species: Chironomus tentans
C;Species: Chironomus tentans
C;Species: Obser-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S08167
R;Paulsson, G:; Lendahl, U.; Galli, J.; Ericsson, C:; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A;Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structanterence number: S08167 MUID:90172404; PMID:1689777
A;Accession: S08167
A;Accession: S08167
A;Accession: DNA
A;Reference with conceptual translation
A;Accession: Compared with conceptual translation
A;Accession: Casterences: GB:X52263; NID:97057; PIDN:CAA36506.1; PID:97058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKGICSCONGATCDSVTGSCECRPGWRGKKCDRPCPDG--RFGEGCNAICDCTTTNDTSM 1109
                                                                                                                                                                                                                                              1110 YNPFVARCDHVTG-ECR------CPAGWTGPDCQTSCPLGRHGE----GCRHSCQ 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QMSPGGCGSGKSFNKLTCQCECDQSASKCGLKRWNADTCKCECQPGMPPEGCGKQTWISD 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                                 123 CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKE
                                                                                                                                                                                                                                                                                                                                                                        183 LGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQT----TSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S--QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLK-----KGKKCSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 CHCPLEAPK--CAPGVGLVRDGCGC-CKVCAKQLNEDCSKTQPCDHTKGLEC----NFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 CICPTAEPAGGCSAPLKWDDDKCSCACPAKWEEKKEKCVESGKIWNPNTCECGCAQLNCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 ASSTALKGICRAQ-SEGRPCEYNSRIYQNGESFQPNCQHQCTCI---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELG
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                                                                                                                                                                                TOP----CDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 4
C,Superfamily: unassigned Balbiani ring proteins
                                               CPAACHCPLEAP-----KCAPG--
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                                                   56
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A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y64GlOA.f. - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27283 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 S;Ainscough, R. Sthinscough, R. Submitted to the EMBL Data Library, September 1999 A;Reference number: Z20336 A;Accession: T27283 A;Accession: DNA A;Accession: Caenoria Caenor
submitted to the EMBL Data Library, October 1998
A;Reference number: 220293
A;Reference number: 220293
A;Reference number: 220293
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-111 vMLL>
A;Cross-references: EMBL:AL032657; PIDN:CAA21739.1; GSPDB:GN00019; CESP:Y47H9C.4
A;Reperimental source: clone Y47H9C
C;Genetics:
A;Gene: CESP:Y47H9C.4
A;Map position: A;Appl: 150/1; 238/3; 342/3; 797/1; 851/1; 947/2; 1017/1; 1083/1
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKKYRPKYCGSCVDGRCCTPQLTRTV------KMRFRCEDGETFSKNVMMIQSCKCNY 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----scpcsdascskolgkclcplgtkgvs 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 CPAACHCPLE-APKCAPGVGLVR-----DGCGCCKVCAK-QLNEDCSKTQPCDHTKGLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSKTCTCVRENTLMCAPNTGFCRCKPGFYGDNCELACSKDSYGPNCEKQAMCDWNHASEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
8.2%; Score 174; DB 2; Length 1111;
Best Local Similarity 19.7%; Pred. No. 4.3e-05;
Matches 84; Conservative 33; Mismatches 161; Indels 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 109;
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8.2%; Score 173.5; DB 2; Length 1620;
Best Local Similarity 24.2%; Pred. No. 6.8e-05;
Matches 92; Conservative 33; Mismatches 146; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 ESCEL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 NCPHAN 363
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Lirombospondin precursor - chicken
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CiAccession: A38804
Cibac: Jobquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-8043, 1991
A;Fitle: Cloning and sequenching of chicken thrombospondin.
A;Reference number: A39804; MUID:91217026; PMID:2022631
A;Accession: A39804
A;Accession: A39804
A;Accession: A39804
A;Accession: A39804
A;Accession: A39804
A;Accession: A39804
A;Accession: Branch
A;Residues: 1-1178 clam>
A;Accession: A39804
A;Accession: A3980
                                                                                                                                                                                    membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 NFGASSTALKGICRAQ----SEGRPCEYNSRIYQNGESF-QPNCQHQCTCIDGAVGCIP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 DQDGLLGKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283
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                                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:AAC26680.1
C;Genetics:
                                                                                                                                                                                 sperm-specific
                                Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 L-CPQELSLPNLGCPNPRLVKVTGQC------CE-----EWVCDEDSIKDPME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #605 SRCLDNNEGNSNCVTYALKCPAHSLYTNCL-----PSCLPSCSDPEGLCGGTSPEVPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----CEPDYV---LSNDKCVPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 TSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPC-----GQPVYS---SLKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4560 ---SECGCKDAHGV-----LIPESKTWVSRGCTKNCTCKGGTVQCHDFSCPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 KKCSKTKKSPE-----PVRFTYAGCLSVKKYRPKYCGSCVD--GRC--CTPQLTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 TRLALSTCPAACHCPLBAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%; Score 152; DB 2; Length 5376; Best Local Similarity 21.0%; Pred. No. 0.0082; Matches 81; Conservative 39; Mismatches 138; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Function:
A;Description: functions in multiple cell adhesion processes
A;Note: found exclusively on the apical region of the sperm head
C;Keywords: cell adhesion
                                                                                C,Accession: T42215
R,Gao, Z.; Garbers, D.L.
B,Biol. Chem. 273, 3421, 1998
A,Hitle: Species diversity in the structure of zonadhesin, A,Reference number: Z22080; MUID:98123114; PMID:9452463
                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5376 <GAO>
sperm-specific membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1659 CKEGCICQSGYVLHKNKCMLRIHCDC 4684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 VKWRFRCEDGETFSKNVMMIQ-SCKC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4539 CEEGCV------
   N:Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 5
                                                                                                                                                                                                                                              A, Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: Zan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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Cyactesion: T13954
RiNakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
RiNakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Rinakayama, M.; Dakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Accession: T13954
A;Residue: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1574 «NAK>
A;Residues: 1-1574 «NAK>
A;Cross-references: EMBL:AB011532; NID:93449293; PIDN:BAA32462.1; PID:93449294
C;Genetics:
A;Gene: MEGF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                             311
                                                                                                                                       312 ----KYCG---SCV----DGRCCTPQLTRIVKMRFRCEDGET-FSKNVMMIQSCKCNYNC 359
                                                                                                                                                                                                 557 EGKQTWCGEACQCICPGGDKNCGNKKFFDKPSCECKCKNNPTCTSPQVWDADDCEC--KC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| |:
AGFQGERCQAEC---ESG-FFGFGCRHRCTCQPG-VACDPVSGECRTQCPPGYQGEDCGQ 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSSPCTCONGGTCDPVLGACRCPPGVSGAHCEDGCPKGFYGKHCRKKCHCANRGRCHRLY 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAC-LCDPGLYGRFCHLACPPWAFGPGCSEDCLCEQ--SHTRSCNPKDGSCS-----CK 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPL-------CPQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- CPNPRLVKVTGQC-CEEWVCDEDSIKDPMEDQDGLLGKELGFDA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----CPACEHGASC------NPETGTCLCLPGFVGSRCQDTCSAGW 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Species: Rattus norvegicus (Norway rat)

Species: Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
Accession: T13954
Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGTGCQIRCACANDG-HCDPTTGRCSC----APGWTGLSCQRACDSGHWGPD----
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    KKSPEPVRFTYAGCLSVKKYRP-

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                      KKGKKCSKT
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                                                                                                                                                                                                                                                           P 360
                                                                                                                                                                                                                                                                                                                  P 615
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                      281
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RESULT 11 T42215 zonadhesin -

F;499-555/Domain: thrombospondin type 1 repeat homology <thr3> F;658-697/Domain: EGF homology <egf></egf></thr3>	Db 702 DPSDCVPGSITYMPNGCCKTCIHNPNNIVPCS 733
Query Match 7.1%; Score 150.5; DB 1; Length 1178; Best Local Similarity 23.0%; Pred. No. 0.0025; Matches 65; Conservative 33; Mismatches 102; Indels 83; Gaps 13;	QY 274 Q-PVYSSLKKGKKGSKTKKSPEPVRPTYAGCLSVKKYRPKYC-GSCVD 319
QY 100 CEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPLCPQELSLFNLGCPNPRLVKVTGQCCE 159 Db 326 CWQDGRVFADSESWIVDSCTKCTCQDSRIVCHQITCPPVSCADPSFIEGECCP 378	Qy 320 GRCCTPQLTRIVKOMRFRCEDGETPSKNVVMIQSCKC 355 174 HGCSCCREERTSVRMVSLDCPDGSKLSHSYTHIESCLC 811
QY 160 EWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGRSLKRLFVFGMEPRI 219 Db 379VCSHSDDSEEGWSPWSDWTKCSVTGGSGTQMRGRSCDVTRSACTGPHI 426	
QY 220 LYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLV 261 Db 427 QTRMCSFKKCDHRIRQDGGWSHWSPWSSCSVTCGVGNITRIRLCNSPIPQMGGKNCVGNG 486	laminin Blk chain precursor - human N;Alternate names: kalinin Bl chain; nicein Bl chain C;Species: Homo sapiens (man) C;Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text change 05-Nov-1999
CY 262 KETRICEVRPC	C;Accession: A53612 R;Gercekb, D.R.; Wagman, D.W.; Champliaud, M.F.; Burgeson, R.E. J. Sicl. Chem. 269, 11073-11080, 1994 A;Title: The complete primary structure for a novel laminin chain, the laminin Blk chai
QY 284 KKCSKIKKSPEPVRFIYAGCLSVKKYRPKYCGSCVDGR-CCTP 325	A;Reference number: A53612; MUID:94209274; PMID:7512558 A;Accession: A53612 A;Status: preliminary A;Molecule type: mRNA
RESULT 13 A42112	A;Residues: 1-1170 <ger> A;Cross-references: GB:L25541; NID:g510702; PIDN:AAA61834.1; PID:g510703 A;Vote: authors translated the codon CGA for residue 124 as Gln, GAG for residue 439 as C;Superfamily: laminin-type EGF-like homology</ger>
<pre>mucin-like peptide MLP 2677 - rat C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus sequence_revision 18-Nov-1994 #text_change 10-Oct-1997 C.Accesion. &4.21.1</pre>	C;Keywords: glycoprotein F;1-17/Domain: signal sequence #status predicted <sig>F;8-110/Product: laminin Blk chain #status predicted <mat>F;0-0-10/Product: laminin Blk chain #status predicted</mat></sig>
C. A. William, L.J.; Khatri, I.A.; Wang, D.; Bennick, A.; Fahim, R.E.; Forstner, G.G.; J. Biol. Chem. 267, 5401-5407, 1992 A. Title: cDNA for the catboxyl-terminal region of a rat intestinal mucin-like peptide.	F:250-312/Jomann: laminin-type KGF-11ke homology <leg3- F:378-427/Domann: laminin-type EGF-11ke homology <leg3- F:430-476/Domann: laminin-type EGF-11ke homology <eg11> F:532-576/Domann: laminin-type EGF-11ke homology <leg2></leg2></eg11></leg3- </leg3-
A.Accession: A42112 A.Accession: A42112 A.Molecule type: nucleic acid; protein	Ouery Match 7.0%; Score 147.5; DB 2; Length 1170; Best Local Similarity 20.9%; Pred. No. 0.0041; Matches 84; Conservative 31; Mismatches 101; Indels 185; Gaps 22;
A. Axperimental source: intestine A. Axperimental source: intestine A. Note: sequence inconsistent with the nucleotide translation A. Note: sequence extracted from WCIBI backbone (NCIB) F94720) C. Sunaefamily: wow Willebrand fastor time or asset homelone	Cy 29 ACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLN
Victorianty, von miliebrand factor type C repeat homology <vwc></vwc>	QY 64 CSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNS 104
Query Match 7.1%; Score 150; DB 2; Length 837; Best Local Similarity 19.2%; Pred. No. 0.0019;	Db 309 AHECQRCDCNGHSETCHFDPAVFAASQGAYGGVCDNCRDHTEGRNCERCQLHYF 362
88; Conservative 40	QY 105 RIYQNGESFQPNCQHQCTC-IDGAVGCIPLCPQBLSLPNLGCPNPRLVKVTGQCCEEWVC 163 Db 363 RNRRPGASIQETC-ISCECDPDGAVAGAPCDPVTGQCVC 400
Db 419 TCPAHRQYQACGPSEEPTCQSSSPKNSTLLVEGCFCPEGTTKPAPGYDVCVKICGCVGPD 478	Qy 164 DEDSIKDPMEDQDGLLGKBLGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNP 223
QY 53CKVC	Db 401 KEH 403
Db 479 NVPREFGEHFEFDCKDCYCLEGGGSGIVCQPKKCARGNLTTCEEDGTYLVVEADPDDKCCN 538 OV 73 TKGLECNFGASSTALKGICPADSEGRPCFVNSR TYONGRS FOO 115	QY 224 LQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEV 269
539 TISCKCDPKRCKAERPSCLLGFEVKSEHVPGKCCPVYSCVFKGVCVHENAEYQPGSFVYS 59	270 RPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLISVKKYRPKYCGSC
116 NCQHQCTCIDGANGCIPLCPQELSLPNLGCPNP-RLVKVTGQCCEEWVCD 1	
Db 599 NKCQDCVCTDSMDNSTQLNVISCTHVP-CNISCSSGFELVEVPGECCKKCQQT 650 Qy 165 EDSIKDPMEDODGLLGKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGM 215	Qy 318 -VDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNY 357 DD 503 GFGGIMCSAAAIROCPD-RTYGDVATGCRACDCDF 536
651 HCIIKRPBQQYIILKPGEIQKNPNDRCTFFSCMKINNQLISSVSNITCPDF 7	
QY 216 EPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCG 273	RESULT 15 T09059

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notch4 - mouse
C;Species: Max musculus (house mouse)
C;Date: 1Jun-1999 #text_change 08-Sep-2002
C;Date: 1Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2002
C;Accession: T09059
R;Rowen, L; Mahairas, G; Qin, S; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Recession: T09059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T19959
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1964 <ROW>
A;Coss-references: EMBL:AF030001; NID:g2564945; PID:g2564947
A;Gene: notch4
A;Map position: 17
A;Gene: notch4
A;Map position: 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
C;Superfamily: notch protein; ankyrin repeat homology; EGP homology
C;Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.4%; Pred. No. 0.0086;
Matches 94; Conservative 28; Mismatches 141; Indels 138; Gaps 24;
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Search completed: April 22, 2004, 17:59:22 Job time : 17.5434 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                   OM protein - protein search, using sw model
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Run on:

April 22, 2004, 17:52:34; Search time 10.5276 Seconds (without alignments) 1884.444 Million cell updates/sec

US-09-495-448A-4 2116 1 MSSRIARALALVVTLIHLTR......ANBAAFPFYRLFNDIHKFRD 381 Title: Perfect score: Sequence:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hom	mus n	rattus	P19336 gallus gall	ratt	BUIL	homod	pos		P28686 gallus gall		P48745 homo sapien	xeno	mus musc			mus m	Q99pp0 rattus norv	095389 homo sapien	homod	mus m			P57999 oryctolagus		mus mus	P35440 gallus gall	rattus	Q90zd5 gallus gall		mus m	Q13751 homo sapien	xenor
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ALIGNMENTS

RESULT 1

CYR6 H	UMAN
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S E	934;
5 5	(Rel. 36, Creat
1 E	10-00T-1990 (Rel. 30, make Bequence update)
DE	in precursor (Cysteine-rich, angiogen
E S	(Insulin-like growth factor-binding protein 10) (GIG1 protein).
Z (CYNEI ON IGERBYIO ON CCNI ON GIGI.
SO	,
36	Bukatjota; Metazoa; Unordata; Cianiata; Verrebiata; buteleoscomi; Mammalia, Entheria, Drimatee, Cianiata; Verrebiata; buteleoscomi;
88	Dageof;
RN	[1]
RP	SEQUENCE FROM N.A.
R.	von der Kar
Z.	mitted (JUN-1997) to the EMBL/GenBank/DDBJ database
2 6	[2]
ι ρ. 14 Χ	SECONICE ROW N. N. P.
5 2	Jav D. Berge-Lefranc J.L. Marsollier C. Meiean C. Taviaux S.
B	Ca P.;
RT	"The human growth factor-inducible immediate early gene, CYR61, maps
RT	
R.	Oncogene 14:1753-1757(1997).
RN	[3]
RP	SEQUENCE FROM N.A.
ž	
æ	Nguyen V.C., Perbal B.;
RT	E
E i	i from th
2	Mol. Pathol. 50:310-316(1997).
Z ([4]
κ. σ. ι	SEQUENCE FROM N.A.
Z i	TISSUE=Placenta;
\$ 2	
7 2	Submitted (JON-1997) to the EMBL/Genbank/Dubd databases.
2 0	W WORL EDITION
4	pi n p vi i
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RP	FROM N.A.
æ	Groll C., Koehrle J., Jakob F.;
R.	"Regulation of hCYR61 by vitamin D, serum and cytokines in fetal human
RI	
7 5	Submitted (UUL-1997) to the EMBL/Genbank/DDBJ databases.
Z Z	SECTIONCE PROM N.A.
Z.	Tai G., Estable M., Liu J., Chow
RŢ	nization and expression of the C
RT.	fibroblasts."; Submitted (SED-2000) to the EMBL/GenBank/DDBL databases.
N.	
쯗	SEQUENCE FROM N.A.

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INTERACTION WITH INTEGRIN ALPHA-V/BETA-6.

RA Greesktewicz T.M., Kirsching D.J., Chen N., Lau L.F.;

KEACION WITH INTEGRIN ALPHA-V/BETA-6.

RA Greesktewicz T.M., Kirsching D.J., Chen N., Lau L.F.;

REACION WITH Integrin alpha vbeta S and enhances mitogenesis through integrin alpha vbeta S and enhances mitogenesis through integrin alpha vbeta I independent of its carboxyl-terminal domain.";

J. Biol. Chem. 276:21943-21950(2001).

C. -- FUNCTION: Promotes cell proliferation, chemotaxis, angiogenesis and cell adhesion. Appears to play a role in wound healing by upcompleting, in skin fibroblasts, the expression of a number of genes involved in angiogenesis, inflammation and matrix remodeling including VEGA-A, VEGA-C, MMP1, MMP3, TIMP1, uPA, PAI-1 and integrins alpha-3 and alpha-5. Cyrel-mediated gene regulation is dependent on heparin-binding through integrin alpha-6/beta-1, adhesion and adhesive signaling through integrin alpha-Vbeta-5 and cell type-decretion through integrin alpha-Vbeta-5.

C. -- SUBNITE: Interaction with integrin is heparin- and cell type-decretion with integrin is heparin- and cell type-decretion with integrin in through integrin is heparin- and cell type-decretion with integrin is heparin- and cell type-decretion with integrin in through integrin is heparin- and cell type-decretion with integrin is heparin- and type-decretion with integrin is heparin- and cell type-decretion with integrin is the parin- and type-decre
TISSUE-Lung, Placenta, and Skin;

XX Strausberg State 
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MEDLINE=20387398; PubMed=10821835;
Chen N., Chen C.-C., Lau L.F.;
"Adhesion of human skin fibroblasts to Cyr61 is mediated through integrin alpha6betal and cell surface heparan sulfate proteoglycans.";
J. Biol. Chem. 275:24953-24961(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION IN WOUND HEALING.
MEDILINE=21601638; PubMed=11584015;
Chen C.-C., Mo F.-E., Lau L.F.,
"The anglogenic factor Cyrel activates a genetic program for wound
healing in human skin fibroblasts.";
J. Biol. Chem. 276:47329-47337(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH INTEGRIN ALPHA-IIB/BETA-3.
MEDLINE-99377072, PubMed=10446209,
Jedsadayanmata A., Chen C.-C., Kteewa M.L., Lau L.F., Lam S.C.;
"Activation-dependent adhesion of human platelets to Cyr61 and
"Activation-dependent adhesion of human platelets to Cyr61 and
Fispl2/mouse_connective_tissue growth factor is mediated through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98112965; PubMed=9446626; Kireeva M.L., Lam S.C., Lau L.F.; "Adhesion of human umbilical vein endothelial cells to the immediate-early gene product Cyr61 is mediated through integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH INTEGRIN ALPHA-V/BETA-3
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J. Biol. Chem. 274:24321-24327(1999).
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SUBUNIT: Interaction with integrins is heparin- and cell-type-dependent and promotes cell adhesion. In skin fibroblasts it

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Gaps
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                                                                                                                                                                                                                                                                                                                           Genew, HONC:2654; CYR61.

MIM, 602369; -.

RGO, GO:000828; P:cell proliferation; TAS.

RGO; GO:0007345; P:embryogenesis and morphogenesis; TAS.

InterPro; IPR006208; Cyg knot.

R InterPro; IPR006207; Cyg knot.

R InterPro; IPR000884; TSP1.

R InterPro; IPR001007; VWP.C.

R Pfam, PF00017; Cyg knot; 1.

R Pfam, PF00019; IRBP; 1.
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L -> I (IN REF. 5).
L -> R (IN REF. 5).
F -> L (IN REF. 7).
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99.5%; Pred. No. 3.1e-155;
iive 1; Mismatches 1;
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CYR61 PROTEIN.
IGFBP.
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CTCK 2; 1.
IGF_BINDING; 1.
                                                                                                                                                                                                                             EMBL, Y11307, CAA72167.1, ---
EMBL, AR03594, AAB61240.1;
EMBL, AR031385, AAB84227.1;
EMBL, 298053; CAB10848.1,
EMBL, BC001271, AAG59863.1,
EMBL, BC001271, AAH01271.1;
EMBL, BC001293, AAH09199.1,
EMBL, BC016952; AAH16952.1,
Genew, HGNC:2654; CYR61.
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VWFC 1; 1.
VWFC 2; 1.
                                                                                                                                                                                                        EMBL, Y12084; CAA72802.1; -. EMBL; U62015; AAB58319.1; -. EMBL; Y11307; CAA72167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00222; IGF BINDI
PROSITE; PS0092; TSP1; 1.
PROSITE; PS01208; VWFC_1; 1
PROSITE; PS50184; VWFC_2; 1
Chemotaxis; Cell adhesTon;
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SMART; SM00121; IB; 1.
SMART; SM0209; TSP1; 1.
SMART; SM0214; VMC; 1.
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Pfam; PF00090; tsp_1; 1
Pfam; PF00093; vwc; 1.
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Matches 379; Conserv
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PROSITE; PS01225;
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KICGIGISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY 300
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                                                                     NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ 120
                                                                                         61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEVNSRIYQNGESFQPNCKHQ 120
                                                                                                                                             CICIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180
                                                                                                                                                                 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180
                                                                                                                                                                                                                   KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCS 240
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MSSRIARALALVVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
                       MEDIATE=20387398; PubMed=10821835;
Chen N., Chen C.C., Lau L.F.;
Threspin alpha ébeta 1 and cell surface heparan sulfate
integrin alpha ébeta 1 and cell surface heparan sulfate
protecolycans.";
J. Biol. Chem. 275:24953-24961(2000).
I. Biol. Chem. 275:24953 cell proliferation, chemotaxis, angiogenesis
and cell adhesion. Appears to play a role in wound healing by upregulating, in skin fibroblasts, the expression of a number of regulating, in skin fibroblasts, the expression of a number of genes involved in angiogenesis, inflammation and matrix remodeling including VEGA-A, VEGA-C, MMP1, MMP3, TIMP1, uPA, PAI-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIR=BALB/C; TISSUE=Fibroblast;
MEDLINE=90.29146; PubMed=2355916;
O'Brien T.P., Yang G.P., Sanders L., Lau L.F.;
"Expression of cyre1, a growth factor-inducible immediate-early gene.";
Mol. Cell. Biol. 10:3569-3577(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61)
CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61)
CYR61 OR IGFB210 OR CCN1.
Mus musculus (Mouse).
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STATAIN-A.J. TISSUB-Embryonic fibroblast,
MEDLINE=91288203; Unbed=202642;
Latinkic B.V., O'Brien T.P., Lau L.F.;
"Promoter function and structure of the gimmediate early gene cyrél.";
Nucleic Acids Res. 19:3261-3267(1991).
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integrins alpha-3 and alpha-5 (By similarity). Cyr61-mediated gene regulation is dependent on heparin-binding (By similarity). Downergulates the expression of alpha-1 and alpha-2 subunits of collagen type-1 (By similarity). Promotes cell adhesion and adhesive signaling through integrin alpha-6/beta-1, cell migration through integrin alpha-1/beta-5 and cell proliferation through integrin alpha-7/beta-3 (By similarity).

-!- SUBUNIT: Interaction with integrins is heparin- and cell-type-dependent and promotes cell adhesion (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: LOW IN KIDNEY, ADDENNAL GLAND, TESTES, BRAIN, AND OWARY, WODERATE IN HEART, UTERUS, AND SKELETAL MUSCLE, HIGHEST
                                                                                                                                                                                                                                                                                                                                                                             -!- DEVELOPMENTAL STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1) IN NORMAL CELLS, AND AT A CONSTANT LEVEL IN RAPIDLY GROWING CELLS.
-!- INDUCTION: By growth factors.
-!- SIMILARITY: Belongs to the COW family.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
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HEPARIN-BINDING.
CTCK.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, FAGES014856A8EE9 CRC64;
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379 AA;
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90.9%; Pred. No. 1.3e-141;
ive 10; Mismatches 19;
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IGFBP.
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InterPro; IPR006208; Cye knot.
InterPro; IPR006209; Cye knot.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR0000867; Insl_gro_fac_pr.
InterPro; IPR001007; VWF C.
Pfam; PF00007; Cye knot. 1.
Pfam; PF000019; ISPD; 1.
Pfam; PF000019; ISPD; 1.
SWART; SW001219; ISPD; 1.
SWART; SW00121; ISP 1.
SWART; SW00121; IS 1.
SWART; SW00121; IS 1.
SWART; SW00121; IS 1.
SWART; SW00121; ISP 1.
PROSITE; PS01225; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; TGF EINDING; 1.
PROSITE; PS01229; IGF EINDING; 1.
PROSITE; PS01208; VWFC_2; 1.
PROSITE; PS01208; VWFC_2; 1.
PROSITE; PS01208; VWFC_2; 1.
PROSITE; PS01208; VWFC_2; 1.
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I muediate early growth regulatory gene CTR61.";

I Biol. Chem. 25:282929836(200).

I Biol. Chem. 25:2829298036(200).

I Biol. Chem. 25:2829298036(200).

I Biol. Chem. 25:2829298036(200).

I Biol. Chem. 25:2829298036(200).

I modulating, in skin fibroblasts, the expression of a number of genes involved in angiogenesis, inflammation and matrix remodeling including VEGA-A, VEGA-C, MMP1, MMP3, TIMP1, UPA, PAI-1 and integrine alpha-3 (By similarity). Cyrci-mediated gene regulation is dependent on heparin-binding (By similarity). Downregulation is dependent on heparin-binding (By similarity). Downregulates the expression of alpha-1 and alpha-2 subunits of collagen type-1 (By similarity). Promotes Cell adhesion and adhesive signaling through integrine alpha-1/beta-5 and cell proliferation through integrin alpha-1/beta-5 and cell proliferation through integrin alpha-1/beta-5 and cell proliferation through integrin alpha-1/beta-5 and cell proliferation through integrine alpha-1/beta-5 and cell shallarity).

I SUBLIMARITY: Contains 1 IGFBP domain.

I SIMILARITY: Contains 1 INFC domain.

I SIMILARITY: Contains 1 INFC domain.
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                                                                                                                                                                                                                                                                                 181 KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ 238
                                                                                                                                                                                                                                                                                                         --LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ 236
                                                                                                                                                                                                                                                                                                                                                                         CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 298
                                                                                                                                                                                                                                                                                                                                                                                                           237 CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYN 358
                                                                                               NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ 120
                                                                                                                                      61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAOSEGRPCEYNSRIYONGESFOPNCKHO 120
                                                                                                                                                                                       CICIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN 356
                                                9
                                    MSSRIARALALVVTLLHITRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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TSSUB-Lung;
MEDLINE=20435857; PubMed=10852911;
Albrecht C., von Der Kammer H., Mayhaus M., Klaudiny J., Schweizer Nitsch R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61)
(Insulin-like growth factor-binding protein 10).
CYR61 OR IGFBP10 OR CCN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPHANEAAFPFYRLFNDIHKFRD 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYR6 RAT
Q9ES72;
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CYR6_RAT
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SEQUENCE
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                                                                                                                                                                                                                                MEDLINE=89145206; PubMed=2537491;
Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
Identification of a phorbol ester-repressible v-src-inducible gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:1178-1182(1989).
-!- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- SIMILARITY: BY V-SRC.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
Gallus.
                                                                                          (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 42, Last annotation update)
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VWFC.
TSP TYPE-1.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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InterPro; IPR006207; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR000867; Intel_gro_fac_pr.
InterPro; IPR0010087; WFC.
Pfam; PP00007; Cys knot; I.
Pfam; PF00019; IGPBP; I.
Pfam; PF00019; IGPBP; I.
Pfam; PF00090; tsp_1; I.
Pfam; PF00090; tsp_1; I.
SWART; SW00119; Tsp_1; I.
SWART; SW00111; IB; I.
SWART; SW00214; VWC; I.
PROSITE; PS01225; CTCK_2; I.
PROSITE; PS01225; CTCK_2; I.
PROSITE; PS01208; VWFC_2; I.
357 CPHPNEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J04496; AAA48661.1; -.
                                                                                                                              CEF-10 protein precursor
                                                                       STANDARD;
                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A41428; A41428
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                            01-NOV-1990
                                                                                                        01-NOV-1990
                                                                                                                    10-0CT-2003
                                                                      CHICK
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P19336;
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Tezuka K., Tamatani T.;

Tezuka K., Tamatani T.;

Tezuka K., Tamatani T.;

Tezuka K., Tamatani T.;

"Rattus norvegicus connective tissue growth factor.";

"Rattus norvegicus connective tissue michatractant secreted by the connective tissue michatractant secreted by the connective tissue michatractan and differentiation of chondrocytes (By similarity). Mediates heparinand differentiation of chondrocytes (By similarity). Mediates heparinand differentiation of chondrocytes (By similarity). Mediates heparinand differentiation of chondrocytes (By similarity). Mediates heparincell for and divalent cation-dependent cell adhesion in many cell types including fibroblasts, endothelial and epithelial cells (By similarity). Enhances fibroblast growth factor-induced cells (By similarity).

"Sumilarity: Belongs to the CCN family.

"SIMILARITY: Contains 1 IGFBP domain.

"SIMILARITY: Contains 1 IGFBP domain.
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                                                                                                                                                                                                                                                                                                                                                        60 LNEDCSKTOPCDHTKGLECNFGASSTALKGICRAGSEGRPCEYNSRIYQNGESFQPNCQH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 QCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLL 179
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Marks S.C. Jr., Owen T.A., Popoff S.N.;
"Cloning the full-length cDNA for rat connective tissue growth factor:
implications for skeletal development.";
J. Cell. Biochem. 77:103-115(2000).
                                                                                                                                                                                                                                                                                   1 MGSAGARP-ALARALICLARLALGSPCPAVCQCPARAPQCAPGVGLVPDGCGCCKVCAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 SKEFGLDASEGELTRNNELIAIVKG-GLKMLPVFGSEPOSRAFENP----KCIVQTTSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 QCSKTCGTGISTRVINDNPDCKLIKETRICEVRPCGQPSYASLKKGKKCTKTKKSPSPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKWRFRCEDGETFSKNVWMIQSCKCNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 PTYAGCSSVKKYRPKYCGSCVDGRCCTPQQTRIVKIRFRCDDGETFTKSVMMIQSCRCNY
                                                                                                                                                                                                                  1 MSSRIARALALVVTLIHLTRLAL-STCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 GKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEP--RILYNPLQGQKCIVQTTSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
                                                                                                                                             Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                      12;
                                                                    Length 375;
                                                                                                                                         Indels
40651 MW; 95F28553BE35D5AE CRC64;
                                                                 80.1%; Score 1695; DB 1; L
81.0%; Pred. No. 1.4e-123;
Live 20; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGF RAT STANDARD; PRT; 347 AA. O9R1E9; O9WVS1; 28-FEB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Connective tissue growth factor precursor.
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                                                                    Query Match
Best Local Similarity 81.0°
Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             norvegicus (Rat)
375 AA;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

REDLINE=22388257; PubMed=12477932;

RETAILSPERT R.D., Feingold B.A., Garcuse L.H., Derge J.G.,

RIAUREST R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A ltschul S.F., Zeeberg B., Euetow K.H., Schaefer C.F., Bhat N.K.,

A ltschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Scares M.B., Poraldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Scares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Rapleton M., NcEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Robat S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Villalon D.K., Muzny D.M., Scdergren B.J., Lu X., Gibbs R.A.,

Rapleton M., Madan A., Young A.C., Shevchenko Y., Buffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rotherch R., Schein J.E., Jones S.J.W., Marra M.A.,

Renerch R., Schein J.E., Jones S.J.W., Marra M.A.,

Renerch R., Schein J.E., Jones S.J.W., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length
FIYAGCLSVKKYRPKYCGSCVDGRCCIPQLIRIVKWRFRCEDGEIFSKNVMMIQSCKCNY 357
                                 MEDLINE=97327410; PubMed=9184077;
Kireeva M.L., Latinkic B.V., Kolesnikova T.V., Chen C.C., Yang G.P.,
Abler A.S., Lau L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99182484; PubMed=10082563;
Babic A.M., Chen C.C., Lau L.F.;
"Fisp12/mouse connective tissue growth factor mediates endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-91229699; PubMed=2029337;
Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;
"Identification of a gene family regulated by transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91363290; PubMed=1888698;
Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
Rystucture, mapping, and Proression of fisp-12, a growth factorinducible gene encoding a secreted cysteine-rich protein.";
Cell Growth Differ. 2:225-233(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abler A.S., Lau L.F.; "Cyrél and Fispl2 are both ECM-associated signaling molecules: "Cyrél and Fispl2 are both ECM-associated signaling metabolism, and localization during development."; Exp. Cell Res. 233:63-77(1997).
                                                                                                                                                                                                                                                                                                                                                                    P29268; Q922U0; 01-DBC-1992 (Rel. 24, Created) 01-DBC-1992 (Rel. 24, Created) 01-DBC-1992 (Rel. 41, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Connective tissue growth factor precursor (FISP-12 protein) (Hypertrophic chondrocyte-specific protein 24).
CTGF OR COLO OF FISP12 OR FISP-12 OR HCS24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                            348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                                         376
                                                                                                                                                                                     326 NCPGDNDIFESLYYRKMYGDM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Cell Biol, 10:293-300(1991)
                                                                                                                         358 NCPHANEAAFPFY--RLFNDI
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                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 ACSKTCGMGISTRVINDNTFCRLEKQSRLCMVRPCBADLEENIKKGKKCIRTPKIAKPVK 265
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SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGKELGFDASEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01225; IGF BINDING; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS501208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CONNECTIVE TISSUE GROWTH FACTOR
IGEBD.
VWFC.
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46.2%; Pred. No. 1.4e-66;
ive 58; Mismatches 107; Indels 4
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HEPARIN-BINDING (BY SCICK.
BY SIMILARITY.
A -> R (IN REF. 2).
T -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR00084; ISPI—fac_pr.
InterPro; IPR000884; TSPI.
InterPro; IPR01007; VWF.C.
Pfam; PF00007; Cys knot; I.
Pfam; PF00107; Cys knot; I.
Pfam; PF00109; Cys knot; I.
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EMBL; AB023068; BAA82125.1; -.
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Best Local Similarity 46.2%
Matches 176; Conservative
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SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00214; VWC; 1.
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35
94
347 AA;
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SEQUENCE FROM N.A.
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                                                                           Query Match
Best Local S:
Matches 178
   DISULFID
DISULFID
DISULFID
                             DISULFID
DISULFID
CONFLICT
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                                                         SEQUENCE
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cell adhesion and migration through integrin alphavbeta3, promotes endothelial cell survival, and induces angiogenesis in vivo.";
Mol. Cell. Biol. 19:2958-2966(1999).

-! FUNCTION: Major connective tissue mitoattractant secreted by vascular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediaces heparinand divalent cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endothelial and epithelial cells (By similarity). Enhances fibroblast growth factor-induced DNA synthesis (By similarity).

-! SUBUNIT: Monomer (By similarity).

-! SUBUNIT: Monomer (By similarity).
                                                                                                                      -! TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).
-! INDUCTION: By growth factors.
-! SIMILARITY: Belongs to the CCN family.
-! SIMILARITY: Contains 1 IGFBP domain.
-! SIMILARITY: Contains 1 TSP type-1 domain.
-! SIMILARITY: Contains 1 TSP type-1 domain.
-! SIMILARITY: Contains 1 C-terminal cystine knot-like (GTCK) domain.
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VWFC.
TSP TYPE-1.
HEPARIN-BINDING (BY SIMILARITY).
CTCK.
                                                                                                                                                                                                                                                                               PROSITE; P891185; CTCK 1; 1.
PROSITE; P801225; CTCK 2; 1.
PROSITE; P800222; IGF EINDING; 1.
PROSITE; P850029; IGF EINDING; 1.
PROSITE; P8501208; VWFC 1; 1.
PROSITE; P850184; VWFC 2; 1.
Cell adhesion; DNA synthesis; Extrac Signal.
SIGNAL.
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1066
1166
342
348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 QHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 KFELSGCTSVKTYRAKFCGVCTDGRCCTPHRITTLPVEFKCPDGEIMKKNYMFIKTCACH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 SOCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCN 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.; "Connective tissue growth factor: a cysteine-rich mitogen secreted by human vascular endothelial cells is related to the SRC-induced immediate early gene product CEF-10."; "cell Biol. 114:1285-1294(1991).
                                                                                                                                                                                                                                                                          1 MSSRIARALALVVTLLHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
                                                                                                                                                                                                                                                                                                   58 KOLNEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFOPNC
                                                                                                                                                                                                                                 Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                            41;
                                                                                                                                                                                , Score 952.5; DB 1; Length 348; Pred. No. 2.1e-66; 57; Mismatches 106; Indels 41
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
E Y SIMILARITY.
E - K (IN REF. 1).
W; 4D786D9089174049 CRC64;
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TISSUE=Umbilical vein endothelial cells;

MEDLINE=9187114; FubMed=1293144;

Igarashi A., Bradham D.M., Okochi H., Grotendorst G.R.;

"Connective tissue growth factor.";

J. Dermatol. 19:642-643(1992).
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TISSUE=Umbilical vein endothelial cells;
MEDLINE=91373462; PubMed=1654338;
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  292 BY
306 BY
322 BY
324 BY
161 E
                                                                                                                                                                                  45.0%;
al Similarity 46.6%;
178; Conservative 5
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  255
272
283
286
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291
161
348 AA;
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366 AFPFY -- RLFNDI 376
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349 AA;
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Best Local Simi
Matches 174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -: SUBCELUIAR LOCATION: Found in the extracellular matrix and as a goluble form (By similarity).

-: SUBCELUIAR LOCATION: Found in the extracellular matrix and as a goluble form (By similarity).

-: ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Long;

Isold=P29279-1; Sequence=Displayed;
Name=2; Synonyms=Short;

Isold=P29279-2; Sequence=VSP 002460;

Note=No experimental confirmation available;

-: SIMILARITY: Contains 1 IGFBP domain.

-: SIMILARITY: Contains 1 VWFC domain.

-: SIMILARITY: Contains 1 VWFC domain.

-: SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22442376; PubMed=12553878;
Ball D.K.; Rachfal A.W., Kemper S.A., Brigstock D.R.;
Ball D.K.; Rachfal A.W., Kemper S.A., Brigstock D.R.;
Ball D.K.; Rachfal A.W., Kemper S.A., Brigstock D.R.;
The heparin-binding 10 kDa fragment of connective tissue growth factor (CTGF) containing module 4 alone stimulates cell adhesion.";
J. Endocrinol. 176:R1-R7(2003).
-!- FUNCTION: Major connective tissue mitoattractant secreted by vascular endochelial cells. Promotes proliferation and differentiation of chondrocytes. Mediates heparin- and divalent cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endothelial and epithalial cells. Enhances fibroblast growth factor-induced DNA synthesis.
                       MEDLINE=97207446; PubMed=9054739; Oemar B.S., Werner A., Garnier J.M., Do D.D., Godoy N., Nauck M., Marz W., Rupp J., Pech M., Luescher T.F.; "Human connective tissue growth factor is expressed in advanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE—Chondrocytes;
MEDLINE=20080294; PubMed=10614647;
MEDLINE=20080294; PubMed=10614647;
Makanishi T., Nishida T., Shimo T.,
Tamacani T., Pazuka K., Takigawa M.;
"Effects of CTGF/Hcs24, a product of a hypertrophic chondrocytes specific gene, on the proliferation and differentiation of chondrocytes in culture.";
Endocrinology 141:264-273(2000).
                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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GO: GO: 0005886; C: plasma membrane; TAS.
GO: GO: 0005586; C: plasma membrane; TAS.
GO: GO: 000551; P: cell intervity and/or maintenance; TAS.
GO: GO: 0008544; P: epidermal differentiation; TAS.
GO: GO: 0008511; P: cesponse to wounding; TAS.
InterPro; IPR006207; CYS. Knot.
InterPro; IPR006207; CYS. Knot.
InterPro; IPR006807; CYS. Knot.
InterPro; IPR006807; CYS. Knot.
InterPro; IPR006807; CYS. Knot.
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EMBL; AL354866; CAC44023.1; -.
                                                                                                                                                                                 atherosclerotic lesions.";
Circulation 95:831-839(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M92934; AAA91279.1; -.
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Genew; HGNC:2500; CTGF.
MIM; 121009; -.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   Cobley
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126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 GISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 VKKYRPKYCGSCVDGRCCTPQLTRTVKARFRCEDGETFSKNVMMIQSCKCNYNCPHANEA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
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9 LALVVILLHLTRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCAKQLNEDCSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 TOPCDHIKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNCOHQCTCIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 AVGCMPLCSMDVRLPSPDCPPPRRVKLPGKCCEEWVCDEP-----KDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 ASEVELTRANELIAVGKGRSLKRL-PVPGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 ------TVVGPALAAYRLEDTFGPDPTMI-----RANCLVQTTEWSACSKTCGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.8%; Score 947; DB 1; Length 349;
llarity 46.6%; Pred. No. 5.6e-66;
Conservative 58; Mismatches 101; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                             TSP TYPE-1.
HEPAZIN-BINDING.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                          POTENTIAL.
CONNECTIVE TISSUE GROWTH FACTOR.
IGFBP.
VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 2).
/FTId=VSP 002460.
D -> H (IN REF. 4).
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38069 MW;
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IGFBP.
338 SLYYRKMYGDM 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                            269 2
284 2
349 AA;
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                                                                                                  CONFLICT
CONFLICT
CONFLICT
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                                          DISULFID
                                                          DISULFID
                                                                                                                                                            SEQUENCE
                                                                           CONFLICT
                                    DOMAIN
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                                                                                                                                                                DNA synthesis; Extracellular matrix; Heparin-binding;
                                                Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                           P. P.
                                                                                                           TISSUB=Aorta;
Lilibensiek B., Lin Z., Fotsis T., Schimanski M., Bierhaus A.,
Kanitz M., Kauffmann G., Schweigerer L., Ziegler R., Nawroth
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL, CONNECTIVE TISSUE GROWTH FACTOR
 O18739; Q9GL71;
15-UUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Connective Lissue growth factor precursor.
CTGF OR CCN2.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF000137; AAB66596.1; --
EMBL, AF309555; AAG30290.1; --
INTERPRO, IPR006208; CQB knot.
INTERPRO; IPR006208; CQB knot.
INTERPRO; IPR000867; INST_Gro_fac_pr.
INTERPRO; IPR000084; TSP1.
INTERPRO; IPR001007; VWF_C.
Pfam; PF00007; Cyg_knot; I.
Pfam; PF00007; Cyg_knot; I.
Pfam; PF00009; tsp_1; I.
Pfam; PF00009; tsp_1; I.
SMART; SM00041; CT; I.
SMART; SM001219; ISP1; I.
SMART; SM00219; TSP1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01185; CTCK 1; PROSITE; PS01185; CTCK 2; 1.

DR PROSITE; PS01022; CTCK 2; 1.

DR PROSITE; PS00022; IGF BINDING; 1.

DR PROSITE; PS00108; VWFC 1; 1.

DR PROSITE; PS01108; VWFC 1; 1.

TW Cell adhesion; DNA synthes*; VWFC 2; 1.

THE SIGNAL CHAIN
                                                                          Bovidae, Bovinae, Bos.
NCBI_TaxID=9913;
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 VGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 TYRAKECGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKSMMFIKTCACHYNCPGDNDIFE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 AFVLLLALCSRPASSQDCSAPCQCPAGPAPRCPAGVSLVLDGCGCCRVCAKQLSELCTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ALVVILIHLIRLALS-TCPAACHCPL-EAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 KYRPKYCGSCVDGRCCTPQLIRIVKWRFRCEDGETFSKNVMMIQSCKCNYNCPHANBAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 SEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Connective tissue growth factor precursor.
Connective tissue growth factor precursor.
Sus scrofa (Pig).
Sus scroda (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
TISSUE=Uterus;
MEDLINE=97390475; PubMed=9242708;
Brigstock D.R., Steffen C.L., Kim G.Y., Vegunta R.K., Diehl J.R.,
Harding P.A.;
WAFC.

HEPARIN-BINDING (BY SIMILARITY).

CYCK.

BY SIMILARITY.

CO -> DC (IN REF. 1).

CV -> YI (IN REF. 1).

CO -> YI (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.4%; Pred. No. 6.7e-65;
Matches 172; Conservative 59; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
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72 DPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGTVYRSGESFQSSCKYQCTCLDGA 130
                                             VGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDA 187
                                                             131 VGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEEWVCDEP-----
                                                                                                                                                                                                                                                                                                                                                 351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Brown leghorn;
MEDLINE=92107157; PubMed=1309586;
                                                                                                                                                                                                                                                       367 FPFY--RLFNDI 376
                                                                                                                                                                                                                                                                        337 ESLYYRKMYGDM 348
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nephroblastomas.";
Mol. Cell. Biol. 1:
-!- FUNCTION: IMMRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADULT KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                 CHICK
                                             128
                                                                                                                       170
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Tactors in uterine secretory fluids. Identification as heparin-binding growth flatform in uterine secretory fluids. Identification as heparin-
Tactors in uterine secretory fluids. Identification as heparin-
Educated Mr 10,000 forms of connective tissue growth factor.";

T. Biol. Chem. 272:2025-2028(1997).

I. FUNCTION: Major connective tissue mitcattractant secreted by vascular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediates heparin-
and divalent cation-dependent cell adhesion in many cell types including fibroblasts, endothelial and epithelial cells (By similarity). Enhances fibroblast growth factor-induced cells (By similarity).

SUBCELLUIAR LOCATION: Found in the extracellular matrix and as a soluble form (By similarity).

SUBCELLUIAR: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 IGFBP domain.

SIMILARITY: Contains 1 TSP type-1 domain.

C. -: SIMILARITY: Contains 1 TSP type-1 domain.

C. -: SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 QPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ALWYTLLHLTRLAL-STCPAACHCPL-EAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AFVILIALCSRPASGODCSGOCOCAAGKRRACPAGVSLVILDGCGCCRLCAKOLGELCTER 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular matrix; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSP TYPE-1,
HEPARIN-BINDING (BY SIMILARITY).
CTCK,
CTCK,
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CONNECTIVE TISSUE GROWTH FACTOR
IGFBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 44.9%; Pred. No. 8.1e-63;
Conservative 57; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB510E2B2B52D4A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.8%; Score 906; DB 1; 44.9%; Pred. No. 8.1e-63;
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SIMILARITY.
SIMILARITY.
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INTERPRO; IPRO06208; Cys_knot.
INTERPRO; IPRO06207; Cys_knot_C.
INTERPRO; IPRO0667; INSI_gro_fac_pr.
INTERPRO; IPRO01004; VWF_C.
INTERPRO; IPRO01007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fram: PF00007; Cys Knot; 1.

Fram: PF00019; Cys Knot; 1.

Fram: PF00019; LGFBP; 1.

Fram: PF00019; LGFBP; 1.

Fram: PF00019; LGFBP; 1.

SMART; SM0011; CT; 1.

SMART; SM0011; LB; 1.

SMART; SM0011; LB; 1.

SMART; SM0011; LB; 1.

SMART; SM0011; LB; 1.

SMART; SM00120; TSP1; 1.

PROSITE; PS01202; TCRC 2; 1.

PROSITE; PS001208; WFC 1; 1.

PROSITE; PS01208; WFC 1; 1.

PROSITE; PS01208; WFC 2; 1.

CCT1 adhesion; DNA synthesis; Ext
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292
349 AA;
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Best Local S:
Matches 167
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DISULFID
SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 KKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANBAA 366
                                                                                              ------KDHTVVGPALAAYRLEDTFGPDPTMM-----RANCLVQTTEWSACSKTCGMG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICATESCUENCE:

TOTAL SECULT BIOL.

TENCTION: IMMEDIATE BARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
FUNCTION: IMMEDIATE BARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
FUNCATION: INTEGLIAND TO THE CONTRACT AND THE WITHOUT SECONDAY
OF NOW GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEP) IS SUFFICIENT
TO INDUCE THE TRANSPORMATION OF CEF IN VITRO.
SUBCELLUIAR LOCATION: Secreted.
TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN
MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN AND
DENERO, IN ADULT CHICKEN.
DENERO, IN ADULT CHICKEN.
DENERO, IN ADULT CHICKEN.
DENERO, IN ADULT CHICKEN.
DENERO, DENEROR SERRESS A HIGH
LEVEL OF NOW GENE WHOSE TRANSCRIPTION IS NORMALLY ARRESTED IN
                                                                                                                                                                                                                                                           217 ISTRVINDNAPCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the CCN family.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 VWFC domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                            247 ISTRVINDNPECRLVKETRICEVRPCGOPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSV
188 SEVELTRINNELIAVGKGRSLKRL-PVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
NOV protein precursor (Nephroblastoma overexpressed gene protein)
NOV OR CCN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Joliot V., Martinerie C., Dambrine G., Plassiart G., Brisac M., Crochet J., Perbal B.;
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                                                                                                                         P42642;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 42, Last annotation update)
NOV protein precursor (Nephroblastoma overexpressed gene protein).
NOV OR CCM3.
Coturnix coturnix japonica (Japanese quail).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----STCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
40.1%; Score 848; DB 1; Length 353;
Best Local Similarity 43.3%; Pred. No. 2.4e-58;
Matches 164; Conservative 45; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWFC.
TSP TYPE-1.
CTCK
BY SIMILARITY.
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY.
BY SIMILARITY.
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IGFBP.
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353 AA;
                                                                                                        NCBI_TaxID=93934;
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DISULFID
DISULFID
                                                                                               Coturnix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 EWSACSKSCGMGFSTRVINRNQQCEMVKQTRLCMMRPCENEBPSD-KKGKKCIQTKKSMK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 AVRFEYKNCISVQIYKPRYCGLCNDGRCCIPHNIKIIQVEFRCPQGKFLKKPMALINICV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG---- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 SWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 AAYRQEATLGIDVSD-----SANCIEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                 61; Gaps
                                                                                                                                                                                                                                                                         VWFC.

TSP TYBE-1.
CTCK.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'-LINKED (GLCMAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 851.5; DB 1; Length 3:
44.0%; Pred. No. 1.3e-58;
ive 44; Mismatches 104; Indels
                                                                                                                                  SMART; SM0209; TDF.,
SMART; SM00214; VWC; 1.
FROSITE; PS01185; CTCK 1; 1.
R PROSITE; PS00225; TGF BINDING; 1.
DR PROSITE; PS01208; VWFC 1; 1.
DR PROSITE; PS01208; VWFC 1; 1.
DR PROSITE; PS01208; VWFC 1; 1.
DR PROSITE; PS0184; VWFC 2; 1.
TOTALO-ONCOGENE; Growth Factor; Signal.
1 24 POTENITAL.
1 24 NOV PROTEIN.
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                             Cys_knot.
Cys_knot_C.
Insl_gro_fac_pr.
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                                                                                                                                                                                                                                                                                                                                                                        38268 MW;
                                      InterPro; IPR006207; Cys_Knot.
InterPro; IPR000867; Insl_gro.
InterPro; IPR000867; Insl_gro.
InterPro; IPR0010017; VWF C.
Pfam; PF00007; Cys_Knot; 1.
Pfam; PF00001; IGFBP; 1.
Pfam; PF00090; IGFBP; 1.
Pfam; PF00090; VWC; 1.
SWART; SM00121; IS; 1.
SWART; SM00121; IS; 1.
SWART; SM00209; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNYNCPHANEAAF 367
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 44.0 tes 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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DISULFID
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  MEDINE=22388257; PubMed=12477932;
A Klauener R.D., Collins F.S., Wagner L.H., Derge J.G.,
A Klauener R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenny B., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenny C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Josden T.B., Toshiyuki S., Carninci P., Prange C.,
B Enownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley V.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                        QLNEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNCQ 118
                                                                HQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGL 178
                                                                                                                                                                                                                        LG------KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQK 228
                                                                                                                                                                                                                                                                                                         CIVOTISWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSK 288
                                                                                                                                                                                                                                                                                                                                        263 TKKSMKAVRFEYKNCTSVQTYKPRYCGLCNDGRCCTPHNTKTIQVEFRCPQGKFLKKPMM 322
67
SLPVLLLLLLLLLLRPSEVNGREAPCPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCAR
                                                                                                                                                                                                                                                                LGGFAMAAYRQEATLGIDVSD-----SSAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
TISSUB-Placenta;
MEDLINE=9436229; PubMed=7520150;
Martinerie - V, Joubert I., Badzioch M., Saunders G.F.,
Strong L.C., Perbal B.;
"Structural analysis of the human nov proto-oncogene and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOV HOWAN STANDARD; FRI; 357 AA.

NOV HOWAN STANDARD; FRI; 357 AA.

01-FEB-1996 (Rel. 33, Created)

10-FEB-1996 (Rel. 33, Last sequence update)

10-CT-2003 (Rel. 42, Last annotation update)

NOV protein homolog precursor (NovH) (Nephroblastoma overexpressed agene protein homolog).

NOV OR CM3 OR NOVH OR IGFBP9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Jiang D., Gou D., Li W.;
"Cloning, sequencing and expression of human nov gene.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 MIOSCKCNYNCPHANEAAF 367
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Oncogene 9:2729-2732(1994),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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A Redigues A.C. Grimwood N. Schmitt J., Weers M.,

Butterfield Y.S.N., Kerzydinki M.I., Skalks U., Shallub D.E.,

A Schmerch A., Schein U.E., Tomes S.J., Warry M. A.,

Butterfield Y.S.N., Kerzydinki M.I., Skalks U., Shallub D.E.,

R. Schmerch A., Schein U.E., Tomes S.J.,

R. Schmerch A., Schein U.E., Tomes S.J.,

R. Merchall and A. Shallub S. Shallub
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Indels
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NOV PROTEIN HOMOLOG.
IGFBP.
VWFC.
TSP TYBE-1.
CTCK.
BY SIMILARITY.
BY 
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39.0%; Score 825.5; DB 1;
Best Local Similarity 41.8%; Pred. No. 1.3e-56;
Matches 158; Conservative 44; Mismatches 113;
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                                                                                                     EMBL; U37063; AAB17096.1; -.
InterPro; IPR006209; Cys kmot.
InterPro; IPR006207; Cys kmot.
InterPro; IPR000867; InsI gro_fac_pr.
InterPro; IPR000884; TSP1.
InterPro; IPR001007; VWF_C.
Pfam; PF00090; Cys kmot; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; tsp_1; 1.
SWART; SW00021; tsp_1; 1.
SWART; SW00121; IB; 1.
PROSITE; PS01185; CTCK_2; 1.
PROSITE; PS01184; VWFC_1; 1.
PROSITE; PS01284; VWFC_2; 1.
PROSITE; PS01284; VWFC_2; 1.
PROSITE; PS0184; VWFC_2; 1.
SIGNAL 1 18 343 NOV PROTEIN DOMAIN 21 355 TTCK TYPE-1
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92 IG
235 IG
235 CT
286 BY
316 BY
316 BY
316 BY
322 BY
320 AM
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285
265
343 AA;
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CARBOHYD
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WEDLINE-96257227; PubMed=8666280;

WINDLINE-96257227; PubMed=8666280;

WINDLINE-96257227; PubMed=8666280;

WINDLINE-96257227; PubMed=8666280;

WINDLINE-100 and Characterization of xnov, a Xenopus laevis ortholog of the Chicken nov gene.";

Gene 171:243-248(1996).

CI - FUNCTION: Immediate-early protein likely to play a role in cell growth regulation (By similarity).

CI - FUNCTION: Immediate carly protein likely to play a role in cell growth regulation (By similarity).

CI - SUBCELLULAR LOCATION: Secreted.

CI - SIMILARITY: Contains 1 IGFBP domain.

CI - SIMILARITY: Contains 1 TyPP type-1 domain.

CI - SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                   123 CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCGEWVCDEDSIXDPMEDQDGLLGKE 182
                                                                                                                                                                                                                                                                                                                                                                                                                               CRDGQIGCVPRCQLDVLLPEPNCPAPRKVBVPGECCEKWICGPD-----EDSLGGLT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 LAAYRPEATL-----GYEVSD-----SVNCIEQTTEWTACSKS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 CGMGFSTRVTNRNRQCEMLKQTRLCMVRPCEQEPEQPTDKKGKKCLRTKKSLKAIHLQFK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 NCTSLHTYKPRFCGVCSDGRCCTPHNTKTIQAEFQCSPGQIVKKPVMVIGTCTCHTNCFK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGISTRVTNDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPH 361
                                                                                                                                                                                                                                  7 RALALWYTLIHLTRLALST -- CPAAC -- HCPLEAPKCAPGVGLVRDGCGCCKVCAKOLNE 62
                                                                                                                                                                                                                                                                           14 OCLCLTFLLLHLLGOVAATORCPPOCPGRCPATPPTCAPGVRAVLDGCSCCLVCARORGE 73
                                                                                                                                                                                                                                                                                                                   DCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCT
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mambibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N -> K (IN REF. 3).
035D5BF4576BD85B CRC64;
                                                                                                                                                                                            39;
                                                                                                                                               Match
Local Similarity 43.1%; Score 827.5; DB 1; Length 357;
Local Similarity 43.1%; Pred. No. 9.3e-57;
Les 157; Conservative 48; Mismatches 120; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
NOV protein homolog precursor (Xnov).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 AA
  BY SIMILARITY.
                                                                                                           MW;
295 333
300 337
97 97
280 280
97 97
357 AA; 39162 M
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P51609;
DISULFID
DISULFID
CARBOHYD
                                                            CARBOHYD
CONFLICT
SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 QPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LALIVITLIHLTRLALSTCPAAC-HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 HFHYKNCTSVQPYKPKFCGQCSDGRCCTPHSTKTMHVBFVCPQKRIVKKPVMVISTCVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KELGFDASEVELTRNNELLAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWS
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SEQUENCE FROW N.A.

SEQUENCE FROW N.A.

SEQUENCE TROWN N.A.

SEQUENCE TROWN N.A.

SEQUENCE TROWN N.A.

STRAIN=C57BL/60; TISSUB=Embryonic head, and Spinal cord;

NEALINE_C57BL/60; TISSUB=Embryonic head, and Spinal cord;

NA SAION N. Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Na Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Na Hadarelli R., Hill D.P. Bult C., Hume D.A., Guackenbush J.,

Baldarelli R., Margin C., Hume D.A., Guackenbush J.,

Baldarelli R., Bradt D., Brusic V., Chothia C., Corbins S.,

Baldare J.A., Bradt D., Brusic V., Chothia C., Corbins J.,

Anala E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Ranai A., Kawaji H., Kawaswa Y., Kedzlerski R.M., King B.L.,

Analott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Naglott D.R., Malteis L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata Y., Taylor M.S., Teasdale R.D., Tomita M.,

Narardo R., Wapner L., Wahlestedt C., Wang Y., Watenaber Y., Wells

Numar Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakaxume N., Sakaxume N.,

Mirayazaki A., Sakaxi D., Shibata K., Shibatas Y.,

Malter A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Myasahi A., Sakaxi D., Sakaxi D., Shibatas K., Shinagawa A.,

Myasaki R., Sakaxi D., Sakaxi D., Shibatas K., Shinagawa A.,

Myasaki A., Sakaxi D., Shibatas K., Shibatas K., Shinagawa A.,

Malter A., Sakaxi D., Shibatas K., Shibatas M.,

Malter A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Materston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; He mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Czech II; TISSUE=Breast tumor; MEDLINE=22388257; PubNed=12477932; Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strauberg R.L., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=97131223; PubMed=8975721;
Snaith M.R., Natarajan D., Taylor L.B., Choi C.P., Martinerie C.,
Shaith M.R., Schoffeld P.N., Boulter C.A.;
Genomic structure and chromosomal mapping of the mouse nov gene.";
Genomics 38:425-428(1996).
                              NOV MOUSE STANDARD; PRT; 354 AA.

064299; 08GA67;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2010 (Rel. 42, Last annotation update)
900 protein homolog precursor (NovH) (Nephroblastoma overexpressed over CCN3.
                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6;
MEDLINE=96204003; PubMed=8622864;
Martinerie C., Chevalier G., Rauscher F.J. III, Perbal B.;
"Regulation of nov by WII: a potential role for nov in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncogene 12:1479-1492(1996).
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nephrogenesis.";
RESULT 14
NOV MOUSE
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SMART; SM00214; VWC; 1.

PROSITE; P801128; CTCK 2; 1.

PROSITE; P800222; IGF BINDING; 1.

PROSITE; P800222; IGF BINDING; 1.

PROSITE; P801208; VWFC 1; 1.

PROSITE; P801208; VWFC 1; 1.
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274 2
351 AA;
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SIGNAL 1
CHAIN 22
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Best Local Simi
Matches 158;
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DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    DCSKTOPCDHTKGLECNFGASSTALKGICRAOSEGRPCEYNSRIYONGESFOPNCOHOCT 122
                                                                                                                                                                                                                                            SCSEMPPCDQSSGLYCDRSADPNNQTGICMV-PEGDNCVFDGVIYRNGEKFEPNCQYFCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                           LALPAYRPEAT------VGVEVSDSSI-------NCIEQTTEWSACSKS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 NCTSLYTYKPRFCGVCSDGRCCTPHNTKTIQVEFQCLPGEIIKKPVMVIGTCTCYSNCPQ 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGISTRVINDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPH 361
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-: SUBCELDUAR LOCATION: Secreted.
-!- SIMELARITY: Belongs to the CCN family.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                            CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCBEWVCDEDSIKDPMEDQDGLLGKE
                                                                                                                              7 RALALVVTLLH-LTRLALS-TCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE
                                                                                                                                                             8 RCLCLGFILFHILSQVSASIRCPSRCPPKCPSISPTCAPGVRSVLDGCSCCPVCARQRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=Sprague-Dawley;
MEDLINE=20035752; PubMed=10570975;
Liu C., Liu X.J., Crowe P.D., Kelner G.S., Fan J., Barry G., Manu F.,
Ling N., De Souza B.B., Maki R.A.;
"Nephroblastoma overexpressed gene (NOV) codes for a growth factor
that induces protein Lyrosine phosphorylation.";
Gene 238:471-478(1999).
-!- FUNCTION: Can act as a growth factor for some cells and binds to a pecific receptor that leads to the phosphorylation of a 221 KDa
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-5CF2-2003 (Rel. 42, Last annotation update)
NOV protein homolog precursor (NovH) (Nephroblastoma overexpressed agene protein homolog).
NOV OR CCN3.
Rattus norvegicus (Rat).
                                                                                        36;
                                             Length 354;
                                        Query Match
38.8%; Score 822; DB 1; Length 35
Best Local Similarity 44.5%; Pred. No. 2.4e-56;
Matches 162; Conservative 46; Mismatches 120; Indels
  OSECESCFC67829DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 AA
  38928 MW;
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354 AA;
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SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 CIDGAVGCIFLCPQELSLPNLGCPNFRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 NCTSLYTYKPRFCGICSDGRCCTPFNIKTIQVSFQCLPGQIIKKPVWVIGTCTCHSNCPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 DCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 LGFDASEVELTRNNELIAVGKGRSLKRLPVPGMEPRILYNPLQGQKCIVQTTSWSQCSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 LALPAYRPEATVGVEL----SDSSI-----SDSSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTGISTRVTNDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 RALALVVTLIHLTRLALST - - CPAAC - - HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.7%; Score 818.5; DB 1; Length ilarity 43.4%; Pred. No. 4.5e-56; Conservative 49; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
NOV PROTEIN HOMOLOG.
IGFBP.
                                                                                                     EMBL; AF171936; AAD49371.1; -.
INTERPRO; IPRO06208; Cyg knot.
INTERPRO; IPRO06207; Cyg-knot.
INTERPRO; IPRO00867; Inal_gro_fac_pr.
INTERPRO; IPRO00864; TSP1.
INTERPRO; IPRO01007; VWF_C.
Pfam; PPO00207; Cyg-knot; 1.
Pfam; PPO00207; LSPEP; 1.
Pfam; PPO0039; Vwc; 1.
SWART; SM00121; IS; 1.
SWART; SM00209; TSP1; 1.
SWART; SM00209; TSP1; 1.
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Search completed: April 22, 2004, 17:57:05 Job time : 11.5276 secs

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Q9WTM9
                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                        Q9wtm9 rattus norv
Q98tx5 xenopus lae
Q9uid7 homo sapien
042607 xenopus lae
Q9tq8 gallus gall
Q9pt80 notophthalm
O97765 sus scrofa
O9558 homo sapien
Q9pse6 gallus gall
Q9pse6 gallus gall
Q9pse6 rattus norv
Q862t0 bos taurus
Q92164 rattus norv
Q9d164 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91v29 mus musculu
Q920w6 mus spicile
Q9vvk0 drosophila
                                                                April 22, 2004, 17:53:04; Search time 38.6013 Seconds (without alignments) 3114.206 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           US-09-495-448A-4
2116
1 MSSRIARALALVVTLLHLTR......ANBAAFPFYRLFNDIHKFRD 381
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                          1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Q9WTX5
Q9UTX5
Q9UTX607
Q9PT80
Q9T164
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sp_virus:*
sp_virus:*
sp_vorlassified:*
sp_rirus:*
sp_rodents:*
sp_bacteriap:*
sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organe!*
sp_phage:*
sp_phage:*
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Maximum DB seq length: 2000000000
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Match Length DB
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1663.5
1938
938
930
91.5
626.5
485.5
373.5
346
334
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336
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Perfect score:
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7 7	QBESA Caenorhabdi Q9xwd6 caenorhabdi Q9nxv1 homo sapien Q86xx4 homo sapien Q9tvq2 caenorhabdi Q94446 chironomus	Q97110 mus musculu Q97574 bos taurus Q97574 bos taurus Q86965 mus musculu Q96404 caenorhabdi Q21281 caenorhabdi Q80614 mus musculu Q92513 mus musculu Q8vea6 mus musculu	Q8spm4 bos taurus Q90z43 gallus gall Q90xg4 gallus gall Q8ciz8 mus musculu Q9cvg8 mus musculu Q8cyg8 mus musculu Q8cyg1 mus musculu
			Q8SPM4 3 Q90Z43 1 Q8CZZ64 1 Q8CZZ6 1 Q9CVG9 1 Q8KOQ1 1 Q8CZ17
470 5 230 4 2327 4 2327 13 70 13		1028 11 1048 13 2048 13 2104 5 360 5 4010 11 406 11 426 11	5146 6 792 13 1095 13 2813 11 482 11 483 11 922 11
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294 195 176 176	174 170 170 170 169	168.5 161.1 161.5	1588.5 1588.5 158.5 156.5 156
7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

ALIGNMENTS

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PRESULT 1

O9WTM9

DYNUM9

DYN
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SMART; SM00121; IB; 1.
SMART; SM00219; TSP1; 1.
PROSITE; SM01219; VWC; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF ENDING; 1.
PROSITE; PS50092; TSPI; 1.
PROSITE; PS01209; VWFC_2; 1.
PROSITE; PS01209; VWFC_2; 1.
SEQUENCE 375 AA; 41460 MW; 78075CA7B380304E CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-107 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 YRLFNDIHKFRD 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRLFNDIHKFRD 375
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Q9UID7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCIDGAVGCIPLCPQBLSLPNLGCPNPRLVKVTGQCCBEWVCDEDSIKDPMEDQDGLLG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 298
                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKKSPEPVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LGFDASEVELTRNNELIATGKGSSLKRLPVFGTEPRVLYNPLHAHGQKCIVQTTSWSQ
                                                                                                                                                                                                                                                                            1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                      61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KELGFDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBSINE:
(01-JUN-2001 (TrEMBLrel. 17, Created)
(01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
(01-JUN-2003 (TrEMBLrel. 15, Last annotation update)
(01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Secreted cysteine-rich protein cyrél.
Xenopus laevis (African clawed frog).
Bukaryots, Metazachs, Chordata; Craniata; Vertebrata; Buteleostomi;
Xenopodinae; Xenopus.
Xenopodinae; Xenopus.
(1) TaxID-8355;
                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Letunkic B.V., Benett B., Smith J.C.;
Letunkic B.V., Benett B., Smith J.C.;
"Characterization of Xenopus cyrfl.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

L. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF220522, AAK00947.1;
-..
GO; GO:0005520; Fiinslin-like growth factor binding; IEA.
GO; GO:0001552; Fiinslin-like growth factor binding; IEA.

R. GO; GO:0001552; Fiinslin-like growth factor binding; IEA.

R. GO; GO:0001552; Fiinslin-like growth; IEA.

R. InterPro; IPR006203; Cys knot.

R. InterPro; IPR006847; IIBI_GYO_fac_pr.

InterPro; IPR000867; IIBI_GYO_fac_pr.

R. Pfam; PF00007; Cys knot; 1.

R. Pfam; PF00009; tsp_l; 1.

R. Pfam; PF00099; tsp_l; 1.

R. Pfam; PF00099; tsp_l; 1.

R. Pfam; PF00099; tsp_l; 1.
                                                                                                                                                                                      Length 379;
                                                                                                                                                                                                                                  Indels
                                                                                          1 24 POTENTIAL.
25 379 CYR61.
379 AA, 41728 MW, D2ABAFD77B84762B CRC64;
                                                                                                                                                                                    Query Match 91.1%; Score 1928; DB 11; Best Local Similarity 90.6%; Pred. No. 1.3e-177; Matches 347; Conservative 11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA
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    PS50092; TSP1; 1.
PS01208; VWFC_1; 1.
PS50184; VWFC_2; 1.
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                                                                      Signal.
SIGNAL
CHAIN
SEQUENCE
    PROSITE; F
PROSITE; F
PROSITE; F
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245 RVINDNSNCRLVRETRICEVRPCGQPSYTSLKKGKKCTKTKKSQAPVRYTYAGCSSVKKY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 RPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFPF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 RPKYCGSCVDGRCCTPQQTRTVKIRFRCEDGETFTYNVYMIQSCRCNYNCPHTNE-AYPY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 VELTRINBELIAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGIST 249
                                                                                                                                            69
                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                188 GELTRRABETVAVIKG-GLRALDVFGSDPQ--SHVVENSKCIVQTISWSQCSKTCGTGIST
                                                                                                                                                                                LAIALLSGFIDLAVSSCPAVCQCPVEVPKCAPGVGLVLDGCGCCKICAKQLNEDCSKTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 RVINDNPECRLYKETRICEVRPCGOPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKY
                                                                                                                                     11 LVVTLLH-LTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
MOSI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
A Anding B., Long Y.,
A Anding D., Long Y.,
I "Cloning of a new gene down-regulated in the small-cell tumor
I "Cloning of a new gene down-regulated in the small-cell tumor
I submitted (WAY-1997) to the EMBL/GenBank/DDBJ databases.
L Submitted (WAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003114; AAP21597.1; -1.
R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0005576; F:insulin-like growth factor binding; IEA.
R GO; GO:0001558; P:risulin-like growth; IEA.
R InterPro; IPR006209; Cys knot.
R InterPro; IPR006809; Cys knot.
R InterPro; IPR0008867; Insl_gro_fac_pr.
R InterPro; IPR000887; Insl_gro_fac_pr.
R InterPro; IPR000887; INSL_GO.
       DB 13; Length 375;
Query Match

78.6%; Score 1663.5; DB 13; Lengt
Best Local Similarity 79.3%; Pred. No. 4.3e-152;
Matches 295; Conservative 29; Mismatches 41; Indels
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24 CNGECQCPNKVPVCDPGVRMVQDGCGCCKVCSKQLGELCTERDVCDPHKGLFCDFGSRVN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 QSRLCMVRPCEADLEENIKKGKKCIRTPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 PNPRLVKW-GOCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 SLKRLPVFGMEPRILYNP---LQGQKCIVQTTSWSQCSKTCGTGISTRVINDNPECRLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 ----LPAFRMEE--TYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 CPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPLCPQELSLPNLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 PFPRRVKLPGKCCEEWVCDQP------OERTLVGPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 ETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 CIPOLIRIVKMRFRCEDGEIFSKNYMMIQSCKCNYNCPHANE--AAFPFYRLFNDI 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 CTPHRIATLPVEFKCPDGEVMKKOMMFIKTCACHFNCPGDNDIFFEAMYYRKMYGDM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLE-1.17, Last sequence update)
01-OCT-2003 (TrEMBLE-1.25, Last annotation update)
01-OCT-2003 (TrEMBLE-1.25, Last annotation update)
Connective tissue growth factor precureor (Connective tissue growth
factor/hypertrophic chondrocyte-specific protein 24).
Gallus gallus (Chicken).
Eukaryota; Metazca; Chordata; Craniata; Verrebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005576, C:extracellular; IEA.
GO; GO:0005520; E:extracellular; IEA.
GO; GO:0005520; F:insulin-like growth factor binding; IEA.
GO; GO:0005581; P:regulation of cell growth; IEA.
InterPro; IPR006209; Cys_knot.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000867; Twsl_gro_fac_pr.
InterPro; IPR00087; Twsl_gro_fac_pr.
InterPro; IPR00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                              44.3%; Score 938; DB 13; Length 3
47.2%; Pred. No. 4e-82;
live 51; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
Mukudai Y., Kubora S., Takigawa M.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AJ298335; CAC33438.1; -
       SMART; SM00041; CT; 1.
SMART; SM00120; TB1.
SMART; SM00214; WG; 1.
SMART; SM00214; WG; 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS0092; TSP1 1.
PROSITE; PS01208; WWFC 2; 1.
PROSITE; PS01208; WWFC 2; 1.
SMO0SITE; PS01208; WWFC 2; 1.
SMOUSITE; PS01208; WWFC 2; 1.
SMOUSITE; PS01208; WWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
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01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 47.2%
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q98TQ8
              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 GCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NGESFOPNCKHOCTCIDGAVGCIPLCFOBLSLPNLGCPNPRLVKVTGQCCEEWVCDEDSI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGSSLKRIPVFGMEPRIRYNPLQGQK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIVQTTSWSQCSKTCGTGISTRVTNDNPECKLVKETRICEVRPCGQPVYSSLKKGKKCSK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCED-----GE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRT-----CEDAVPLRRWGD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GCGTHPNLCIHLGHTASPTSYKHHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGESFOPNCOHOCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDPMEDQDGLLGKELGPDASEVELTRNNELIAVGKGRSLKRLPVFGMEPRILYNPLQGQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Connective tissue growth factor XCTGF.
Xenopus laevis (African clawed frog).
Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ying Z., King M.L.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 143524; AAB67639-1; --
R GG, GG:000554; AAB67639-1; --
R GG; GG:0005556; G:extracellular; IEA.
GG; GG:0005556; G:extracellular; IEA.
GG; GG:0005550; F:insulin-like growth factor binding; IEA.
GG; GG:0005550; F:insulin-like growth; IEA.
GG; GG:0005520; F:insulin-like growth factor binding; IEA.
R GG; GG:0005520; F:insulin-like growth; IEA.
R InterPro; IPR006209; Cyg knot.
R InterPro; IPR000867; Insl_Gro_Fac_pr.
R InterPro; IPR000867; Insl_Gro_Fac_pr.
R InterPro; IPR000097; VWF_C.
R Ffam; PF00007; VWF_C.
R Ffam; PF00007; VWF_C.
R Ffam; PF000091; IGFBB; 1.
R Ffam; PF00091; VWG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 334;
Pfam; PF00007; Cys knot; 1.

Pfam; PF00219; IGFBP; 1.

Pfam; PF00090; tsp_1; 1.

Pfam; PF00093; vwc; 1.

SMART; SM00204; CT; 1.

SMART; SM00204; Vwc; 1.

SMART; SM00214; Vwc; 1.

PROSITE; PS01225; CTCK_2; 1.

PROSITE; PS01208; VwFC_1; 1.

PROSITE; PS01208; VwFC_2; 1.

PROSITE; PS01208; VwFC_2; 1.

PROSITE; PS01208; VwFC_2; 1.

SEQUENCE 334 AA; 37246 MW; 9188987A7352E948 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 1587; DB 4; Length 33
85.8%; Pred. No. 9.2e-145;
ive 5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 TFSKN----VMMIQSCKCNYNCPHANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 IFQERHDDPVL----KCNYNCPHANEAAFPFYRLFNDIHKFRD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 85.8
Matches 295, Conservative
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Connective tissue growth factor
MEDLINE=99033008; PubMed=9813273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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MYYRKMYGDM 346
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Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AKEQTAVGPALAAYRLEDTYGPDPTMM-----RANCLVQTTEWSACSKTCGM 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEA 365
                                                                                                                                                                                                                                                                                                                                                                                                  127 AVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 VKTYRAKFCGVCTDGRCCTPHRTATLPVEFKCPDGEIMKRKMMFIKTCACHYNCPGDNDI 330
                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                  8 ALALVVTLLHLTRLALSTCPAACHCPL-EAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSK
                                                                                                                                                                                                                                                                                                                    7 AVALLLALLG-PEVRGQECSGQCQCGSGPGPSCPAGVSLVLDGCGCCRVCAKQLGELCTE
                                                                                                                                                                                                                                                                                                                                               67 TQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDG
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Notophthalmus viridescens (Eastern newt) (Triturus viridescens). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.
                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                              CONNECTIVE TISSUE GROWTH FACTOR 69E639AF69BF1D00 CRC64;
                                                                                                                                                                                                                                         DB 13; Length 344;
                                                                                                                                                                                                                                      Query Match
44.0%; Score 930; DB 13; Length 3.
Best Local Similarity 45.3%; Pred. No. 2.4e-81;
Matches 169; Conservative 59; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 AA
                                                                                                                                                                                   POTENTIAL.
                         Pfam; PF00093; vwc; 1.
SWART; SM00041; CT; 1.
SWART; SM00121; IB; 1.
SWART; SM00209; TSP1; 1.
SWART; SM00214; vwc; 1.
SROSITE; PS01185; CTCK 1; 1.
PROSITE; PS00222; IGF BINDING; 1.
PROSITE; PS00222; IGF BINDING; 1.
PROSITE; PS01084; VWFC 1; 1.
PROSITE; PS01084; VWFC 1; 1.
                                                                                                                                                                                                              37499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 AFPFY -- RLFNDI 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Forelimb blastema;
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TISSUE=Forelimb blastema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                   21
344
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Submitted (JAN-2000)
                                                                                                                                                                                                            344 AA;
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                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
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Q9PT80 Q9PT80;

RESULT 6
109 PT80
209 PT80
209 PT
AC 099 PT
DT 01-M
DT

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129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 EVELTRNNELLAVGKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --EQTRVGPALAV----YRQEETYGPD----SSLMRANCLVOTTEWSACSKTCGMGIS
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                                            target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 347;
MEDINE=99033008; FURGES=93273;

X Cash D.B., Gates P.B., Imckawa Y., Brockes J.P.,
Indentification of newt connective tissue growth factor as a tretinoid regulation in lumb blastenal cells.";
If Gene 222.116-124[1498].

E WHIL, AJ271167; CAB65965.11;

R GO; GO:0005276; C:extracellular; IEA.
R GO; GO:0005276; C:extracellular; IEA.
R InterPro; IPR005007; Cys knot.
R InterPro; IPR005007; Cys knot.
R InterPro; IPR001007; VWF.C.
R Pfam; PF00070; Cys knot; I.
R Pfam; PF00070; Cys knot; I.
R Pfam; PF00070; Cys knot; I.
R SWART; SW00029; TSP; I.
R SWART; SW00229; TSP; I.
R PROSITE; PS01228; CTCK 1; I.
R PROSITE; PS01228; CTCK 2; I.
R PROSITE; PS01229; VWC; I.
R PROSITE; PS01209; VWFC; I.
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43.1%; Score 912.5; DB 13; Length
Best Local Similarity 45.1%; Pred. No. 1.2e-79;
Matches 167; Conservative 54; Mismatches 112; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 ISTRVTNDNASCRLEKQSRLCHVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 OPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGCIPLCPQELSLPNLGCPNPRLVKVTGQCCBEWVCDEDSIKDPMEDQDGLLGKELGFDA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSV 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 VGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCEWVCDEP----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEVELTRNNELIAVGKGRSLKRL-PVFGMEPRILYNPLØGQKCIVQTTSWSQCSKTCGTG
                                                             Harding P.A., Brigstock D.R., Cloning and sequencing of a porcine connective tissue growth factor (CTGF) cDNA.";
 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                               EMBL; U70060; ABD00174.1; -.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005520; F:insulin-like growth factor binding; IEA.

GO; GO:00005520; F:insulin-like growth factor binding; IEA.

GO; GO:0001580; P:regulation of cell growth; IEA.

R InterPro; IPR006209; Cyg knot.

R InterPro; IPR00687; IIA91 gro_fac_pr.

R InterPro; IPR000887; IIA91 gro_fac_pr.

R Pfan; PF0000987; IIA91 gro_fac_pr.

R Pfan; PF00009; tsp_1; 1.

R Pfan; PF00009; tsp_1; 1.

R SWART; SW0001; ISP; 1.

R SWART; SW00209; ISP; 1.

R SWART; SW00209; ISP; 1.

R SWART; SW00209; ISP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.5%; Score 878; DB 6; Length 345
Best Local Similarity 43.3%; Pred. No. 2.5e-76;
Matches 161; Conservative 60; Mismatches 111; Indels
                                                                                                        Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                  35AB4275AC1D4B3A CRC64;
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O95958;
01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                          PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF BINDING; 1.
PROSITE; PS01009; TSPI; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_2; 1.
SEQUENCE 349 AA; 37946 MW; 35AB
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ESLYYRKMYGDM 348
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Eukaryota, Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                               SEQUENCE FROM N.A.
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095958
ID 09595
AC 09595
DT 01-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 RYETGVCACKSVG--CEFNOVHYHNGQVFQPNPLFSCLCVSGAIGCTPLF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 ----IPKLAGSHC----EPLLQQLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 RLCYIOPCDSNILKTIKIPKGKTCQPTFQLSKAEKFVFSGCSSTQSYKPTFCGICLDKRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 CPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 CHWPCKCPQQKPRCPPGVSLVRDGCGCCKICAKQPGEICNBADLCDPHKGLYCDYSVDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 CPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 RSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 TSYKTMPAYRNLPLI-----WKKKCLVQATKWTPCSRTCGMGISNRVTNENSNCEMRKEK
                                                                                                                                                                                                                                                                                                                             TISSUE-Mammary gland;
van Golen K.L., Davies S., Wu Z.F., Wang Y.F., Bucana C.D., Root H.,
Chandrasekharappa S., Strawderman M., Ethier S.P., Merajver S.D.;
A novel putative IGF-binding, Lumor suppressor protein, LIBC, and
Rhoc GTPase, are determinants of the inflammatory breast cancer
                                                                                                                                                     ....... Dubertone (Merazoa) Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenotype.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP14879; AAD31517.1;
R GO; GO:0005579; AAD31517.1;
R GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000558; P:insulin-like growth factor binding; IEA.
R GO; GO:000558; P:regulation of cell growth; IEA.
R InterPro; IPR006607; Cyg_knot.
R InterPro; IPR000607; Insl_gro_fac_pr.
R InterPro; IPR000607; Insl_gro_fac_pr.
R InterPro; IPR000804; TSP1.
R Pfam; PF00019; IGFBP; 1.
R Pfam; PF00019; IGFBP; 1.
R Pfam; PF00019; IGFBP; 1.
R SMART; SM0011; IE; 1.
R SMART; SM00121; IE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.6%; Score 626.5; DB 4; Length 331; 36.2%; Pred. No. 4.5e-52; ive 50; Mismatches 118; Indels 47;
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lost in inflammatory breast cancer tumor suppressor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36909 MW; D109C2FDCA1DF549 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Potential IGF binding protein (Fragments).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS00222; IGF BINDING; 1.
PROSITE; PS0092; TSFI; 1.
SEQUENCE 331 AA; 36909 MW; DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 36.23
Matches 122; Conservative
                                                                                                                                       sapiens (Human)
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Q9PSS6
ID Q9PSS
AC Q9PSS
DT 01-M
DT 01-O
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SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
          Pfam; PF00093; vwc; 1.
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121 YGDM 124
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              RERETES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 ASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPLCPQELSLP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 PEDGGGGAGIC----EGDNCVFDGMIYRNGEIFQPSCKYQCTCRDGQIGCLPRCNLGLLLP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 NLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAV 201
                                                                                                                                                                                                                            MEDILINE=92096811; PubMed=1756408;

A Martinerie C., Perbal B.;

A Martinerie C., Perbal B.;

Martinerie C., Perbal B.;

Martinerie C., Perbal B.;

T. Expression of a gene encoding a novel potential IGF binding protein

In human tissues.";

C. R. Acad. Sci., III, Sci. Vie 313:345-351(1991).

G. G. G. G. C. Extracellular; IEA.

G. G. G. G. C. Extracellular; IEA.

G.;

G. G. G. G. F. Hardlation of cell growth, IBA.

R. G.;

G. G. G. G. S.;

R. InterPro, IPR001007; VWF_C.

R. SMART; SM00121; IB; 1.

R. SMART; SM00121; IB; 1.

R. SMART; SM01208; VWF_C.

R. PROSITE; PS001208; VWF_C.

R. PROSITE; PS001208; VWF_C.

R. PROSITE; PS001208; VWF_C.

R. PROSITE; PS001208; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AACPRPCGGRCPAEPPRCAPGVPAVIDGCGCCLVCARQRGESCSPILPCDESGGLYCDRG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 STCPAAC--HCPLEAPKCAPGYGLVRDGCGCCKYCAKQLNEDCSKTQPCDHTKGLECNFG 81
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Jia J.D., Sedlaczek N., Bauer M., Wiecher D., Boigk G., Cho J.J.,

Jia J.D., Sedlaczek N., Schuppan D.,

Ruchl M., Riecken E.O., Schuppan D.,

"Connective tissue growth factor is produced by hepatic stellate cells
and upregulated in rat liver fibrosis.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ236872; CAB41996.1;

InterPro; IPR00084; ISPI.

InterPro; IPR000907; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GPDCPFPRKIEVPGECCEKMVC-----DPRDEV--LLG-------
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 GKGRSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
22.9%; Score 485.5; DB 13; Length
Best Local Similarity 40.2%; Pred. No. 8.9e-39;
Matches 94; Conservative 21; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18656 MW; 4FA69FFDB79B1C67 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 15
176 17
176 AA;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NON CONS
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SEQUENCE
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209R2C
AC 09R2C
AC 09R2C
DT 01-MA
DT 0
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A EDULNE=22549902; PubMed=12658628; A MEDINE=22549902; PubMed=12658628; A EDINATE H. Kateruma S., Kizaki K., Patel O.V., Nakano H., A Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y., Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y., Takahashi T., Imai K., Hisasawa A., Shiojima S., Ikawa H., Suzuki Y., Taujimoto G., Izaike Y., Todoroki J., Hashizume K.; Taujimoto G., Izaike Y., Todoroki J., Hashizume K.; Todaracterization of gene expression profiles in early bovine T. Pregnancy using a custom CDNA microarray."; Mol. Reprod. Dev. 65:9-18(2003).

R EMBL; AB098897; BAC56387.1; ---
R InterPro; IPR006207; Cya-knot.
R InterPro; IPR006207; Cya-knot.
R Pfam; PF00007; Cys-knot; 1.
R PROSITE; PS01185; CTCK_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        214
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                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                    156 OCCREWYCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAYGKGRSLKRL-PVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 NPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYC
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similar to connective tissue growth factor precursor (Fragment).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                  35;
                                                                                                           Query Match
17.7%; Score 373.5; DB 11; Length 128;
Best Local Similarity 43.4%; Pred. No. 4e-28;
Matches 69; Conservative 21; Mismatches 34; Indels 35;
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16.4%; Score 346; DB 6; Length 12
Best Local Similarity 46.0%; Pred. No. 1.8e-25;
Matches 57; Conservative 26; Mismatches 39; Indels
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                                   F30142D0C491B7C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 MEPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 PDPINM-----RANCLVQTTEWSACSKICGMGISTRVIN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
128 128
128 AA; 13803 MW;
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Query Match
15.9%; Score 337; DB 4; Length 10
Best Local Similarity 40.0%; Pred. No. 1e-24;
Matches 64; Conservative 17; Mismatches 19; Indels
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                             216 BPRILYNPLQGQKCIVQTTSWSQCSKTCGTGISTRVTNDN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TEWSACSKTCGMGISTRVTNDN 100
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
FISP-12.
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InterPro; IPR006207; Cys knot_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB039096; BAB68620.1; -. AB039097; BAB68621.1; -. AB039098; BAB68622.1; -.
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AB039101; BAB68625.1;
AB039102; BAB68626.1;
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PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01225; CTCK 2; 1.
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hes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local S:
Matches 56
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ISTRVINDNIFCRLEKQSRLCMVRPCBADLEENIKKGKKCIRTPKIAKPVKFELSGCTSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Suppression subtractive hybridization identifies high glucose levels as a stimulus for expression of connective tissue growth factor and other genes in human mesangial cells.";

EMBL, AF079531; AAD02838.1; -.

InterPro; IPR066208; Cys knot.

InterPro; IPR066208; Cys knot.

InterPro; IPR06620; Cys knot.

INTERPROSED:

IN
                                                                                                                                                            01-MAY-1999 (TrEWBLrel. 10, Created)
01-MAY-1999 (TrEWBLrel. 10, Last sequence update)
01-MAX-2003 (TrEWBLrel. 23, Last annotation update)
Connective tissue growth factor (Fragment).
Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92096871; PubMed=1756408; Martinarie C., Perbal B.; Martinarie C., Perbal B.; Martinarie C., Perbal B.; in human tissues."; C. R. Acad. Sci., III, Sci. Vie 313:345-351(1991). InterPro; IPR001007; VWF.C. SNART; SM00324; VWC, 1. PR0SITE; PS01208; VWFC. 1: PROSITE; PS01208; VWFC. 1: PROSITE; PS01208; VWFC. 1: PROSITE; PS01208; VWFC. 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=93150373; Pubwed=10026205;
Murphy M., Godson C., Cannon S., Kato S., Mackenzie H.S., Martin F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
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16.1%; Score 341; DB 11; Length 113;
Best Local Similarity 55.1%; Pred. No. 4.8e-25;
Matches 59; Conservative 17; Mismatches 31; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIYRAKFCGVCIDGRCCIPHRITILPVEFKCPHGBIMKKNMMFIKIC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 KKYRPKYCGSCVDGRCCTPQLTRIVKMRFRCEDGETFSKNVMMIQSC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
12767 MW; 23EA69FC0A60635E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA; 10813 MW; C64EE2B9AD8A3299 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9UDE;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Potential IGF binding protein (Fragments).
                                                                                                         113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 100 AA
                                                                                                     PRT;
                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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NON TER
SEQUENCE
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96 BGRPCEYNSRIYQNGESFQPNCQHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTG 155
                                                                                                                                                                                                                   156 QCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGRSLKRLPVFGM 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Various strains;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
Liu Y., Kitano T., Roide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Difference among Gene Genealogies of 21 Nuclear Genes of Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-pgn2;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
Five Mus musculus subspecies.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB039094; BAB68619.1;
EMBL; AB0390955; BAB68619.1;
EMBL; AB0390955; BAB68619.1;
                                                                                                                   1 DGAPCIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFPRRVKLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.9%; Score 336; DB 11; Length 119; 47.9%; Pred. No. 1.5e-24; ive 23; Mismatches 36; Indels
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262 KETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCLSVKKYRPKYCGSCVDGR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KOSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 CCTPQLTRTVKMRFRCEDGETFSKNVVMIQSCKCNYNCPHANEAAFPFY--RLFNDI 376
                                                  322 CCTPOLIRIVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFPFY--RLFNDI 376
                                                                                   62 CCTPHRITILEVEFKCPDGEIMKKNWMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ju Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N., Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 CCTPHRITILDVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                Mus spicilegus (Steppe mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
VCBI_TaxID=10103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
15.9%; Score 336; DB 11; Length 119;
Best Local Similarity 47.9%; Pred. No. 1.5e-24;
Matches 56; Conservative 23; Mismatches 36; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB039103; BAB66627.1;
InterPro; IPR006208; Cys_Knot.
InterPro; IPR006207; Cys_Knot_C.
Pfam; PF00007; Cys_Knot_1.
SMART; SM00041; CT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AA; 13626 MW; C7C8AD253DF331CE CRC64;
                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                    119 AA.
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00041; CT7 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01225; CTCK 2; 1.
NON TER 1 13626 MM
                                                                                                                                                                                                                                                                                                                                                            FISP-12 protein (Fragment).
FISP-12.
                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                  Q920W6
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Search completed: April 22, 2004, 17:58:35 Job time : 39.6013 secs

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

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Sequence 2, Appli
Sequence 14, Appl
Sequence 17, Appl
Sequence 25, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 21, Appli
Sequence 21, Appli
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Sequence 36, Appli
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Sequence 36, Appli
Sequence 37, Appli
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Best Local Similarity 100.0%; Pred. No. 5e-170;
Matches 379; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08468847B
Fatent No. 5780263
GENERAL HERETORN:
TITLE OF INVENTION:
TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
ADDRESSEE: CACCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
STATE: NEW JERSEY
COUNTRY: USA
                   US-08-468-847B-14
US-08-468-847B-16
US-08-253-316-25
US-09-182-145-3
US-09-182-145-6
US-09-182-145-6
US-09-182-145-8
US-09-182-145-2
US-09-182-145-2
US-09-182-145-2
US-09-182-145-11
US-09-182-145-12
US-09-182-145-12
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US-09-182-145-13
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 138M FS/2
COMPUTER: 138M FS/2
COMPUTER: 138M FS/2
COMPUTER: 138M FS/2
COMPUTER: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/468,8478
FILING DATE: 6 June 1995
CLASSIFICATION: 435
RECISTRATION DATA:
APPLICATION UNMER: 33,073
REFERENCE MOMBER: 33,073
REFERENCE MOMBER: 33,073
REFERENCE MOMBER: 33,073
REFERENCE COMPUTING: 201-994-1700
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1700
TELEPHONE: COLORS SEQ ID NO: 11:
SEQUENCE CHARACTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 379 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-468-8478-11
    JS-08-468-847B-11
  758.5
758.5
622
622
622
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                                                                                                                                                    April 22, 2004, 17:54:44; Search time 16.4566 Seconds (without alignments) 1188.962 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                              US-09-495-448A-2
2103
1 MSSSTFRTLAVAVTLIHLTR......PNEASFRLYSLFNDIHKFRD 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-142-569-2
US-09-348-815-2
US-09-348-815-2
US-08-468-8478-12
US-08-468-8478-13
US-08-582-337-2
US-09-582-337-2
US-09-582-337-2
US-09-142-569-6
US-09-142-569-6
US-08-167-628-2
US-08-167-628-2
US-08-167-628-2
US-08-167-628-2
US-08-167-628-2
US-08-167-628-2
US-08-167-628-2
US-08-168-2
US-08-044-368-2
US-09-094-274-2
US-09-097-179-2
US-09-097-179-2
US-09-097-179-2
US-09-053-316-2
US-09-05-318-2
US-09-05-318-2
US-09-05-318-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-187-478-2
                                                                                                                                                                                                                                                                                                                                                                                                             389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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Result

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0; Gaps

120

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241 CGTGISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG 300
                                                                                                                                                                         61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
                                                                                                                                                                                                                          121 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWYCDEDSIKDSLDDQDDLLG 180
                                                                                                                                                                                                                                                                        121 CTCIDGAVGCIPLCPQELSLPNÍGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG 180
                                                                                                                                                                                                                                                                                                                                                             181 LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKS 240
                                                                                                                                                                                                                                                                                                                                                                                                             241 CGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
                                                                                       1 MSSSTFRTLAVAVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                     61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNCKHO
                                                                                                                                                                                                                                                                                                                      LDASEVELTRNNELIAIGKGSSLKRLPVPGTEPRVLFNPLHAHGGKCIVQTTSWSQCSKS
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TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/348,815

FILING DATE: 08-Jul-1999

CLASSIFICATION: «Unknown»

ATTORNEY/AGENT INFORMATION:

NAME: JONATHAN L. KLEIN

REGISTRATION NUMBER: 41,119

REGISTRATION NUMBER: 41,119

REGISTRATION NUMBER: PF126PID1

TELECOMMUNICATION INFORMATION:
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.2%; Score 1938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TOPOLOGY: Inhear ;
NOLECULE TYPE: protein ;
SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-348-815-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09348815
Patent No. 6534630
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 NEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 NEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 381 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 301-309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
  Conservative
  379;
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US-09-348-815-2
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                                                                                    61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAGSEGRPCEYNSRIYONGESFOPNCKHO 120
                                                                                                                                   CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG 180
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                                                                                                                                                                                                                                                                                                                                                               CGIGISTRVINDNPECRLVKEIRICEVRPCGQPVYSSLKKGKKCSKIKKSPEPVRFIYAG 300
                                                                                                                                                                                                                                                                                                                                                                                                             CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
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TITLE OF INVENTION: Extracellular Matrix Signalling Molecules NUMBER OF SEQUENCES: 1.7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY; misc feature; OTHER INFORMATION: "Mouse Cyr61 amino acid sequence'; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-142-569-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2103; DB 4; Length 379; Pred. No. 5e-170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 Sears Tower, 233 SOUTH MECKEL DILVE
CTITY. CLALGAGO
STATE: Illinois
COMPUTE: Illinois
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-APP-1999
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
RETERRACY/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28,107
TELEPRONE: 312/474-6300
TELEPRONE: 312/474-6300
TELEPRONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09142569
Patent No. 6413735
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
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Best Local Similarity
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                                                                                                                  Length 381;
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Patent No. 5780263

GENERAL INFORMATION:

APPLICANT Hastings, Gregg A. and Adams, Mark D.

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE: CARELLA BYRNE, BAIN, GILFILIAN,

ADDRESSE: CECCHI, STEWART & OLSTEIN

STREET: BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

COUNTRY: USA
                                                                                                               Query Match 91.7%; Score 1929; DB 4; I
Best Local Similarity 90.9%; Pred. No. 2.6e-155;
Matches 348; Conservative 10; Mismatches 19;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-142-569-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/468,847B
6 June 1995
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: SAS/2
COMPUTER: SAS/2
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,847
FILING DATE: 6 June 1995
CLASSIFICATION: 435
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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFRENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-468-847B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRIVKMRFRCEDGETFSKNVMMIQSCKCNYN 358
                                                                                                                                                                                                                                                 61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
                                                                                                                                                                                                                                                                                                                                                                                          CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL-- 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296
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                                                                                                                                                                      1 MSSRIARALALVVILLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
                                                                                                       1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                            Gaps
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TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: "Human Cyr61 amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: 111nois
COUNTX: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC
   91.4%; Pred. No. 4.5e-156;
ive 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 CPHPNEASFRLYSLFNDIHKFRD 379
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Patent No. 6413735
GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                            Conservative
       Best Local Similarity
Matches 350; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-142-569-4
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121 CICIDGAVG-CIPLCPORISLPNIGCPNPRLVKVSGQCCREWVCDEDSIKDSLDDQDDL- 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKWRFRCBDGEMFSKNVMMIQSCKCNY 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NEDCRKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFQPNCKHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSSRIVRELALVVTLLHTTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                    86.2%; Score 1812.5; DB 2; Length 375; 88.0%; Pred. No. 1.8e-145; ive 10; Mismatches 28; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDG
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TITLE OF INVENTION: Human CCN-Like Growth Factor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CRCELLA, BYRNE, BAIN, GILFILIAN,
ADDRESSEE: CRCCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHTARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,847B
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-468-847B-13
; Sequence 13, Application US/08468847B
Patent No. 5780263
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IEM PS/2
OPERATING SYSTEM: MS-DOS
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 375 AMINO ACIDS
TYPER: AMINO ACIDS
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 NCPHPNEASFRLYSLF 371
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Matches 331; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NEDCRKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFOPNCKHO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 ---LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCSXTCGTGISTRVTNDNPECRLVXETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRIVKMRFRCEDGEMFSKNVMMIQSCKCNY 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fryadcisvkkykpkycdscvbdkccrpolrkrykwkepcepderfskyvwmiosskony 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CICIDGAVG-CIPLCPQELSIPNIGCPNPRIVKVSGQCCBEWVCDEDSIKDSLDDQDDL- 178
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                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                       Length 374;
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APPLICANT: LI, ET AL.
TITLE OF INVENTION: Connective Tissue Growth Factor-2
INTHE OF INVENTION: Connective Tissue Growth Factor-2
INTHE OF INVENTION: Connective Tissue Growth Factor-2
INTHE OF SEQUENCES: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CARELLA, BYRNE, CALTY: NOSICHAN TOND
STREET: 6 BECKER FARM ROAD
CITY: NOSICHAN TARSEY
COUNTRY: USA
ZIP: OTO68
COMPUTER: NEW JERSEY
COMPUTER: 1BM PS/2
COMPUT
                                                                                                                                                                                                                    Ouery Match

86.5%; Score 1819.5; DB 1, Length
Best Local Similarity 88.3%; Pred. No. 4.7e-146;
Matches 332; Conservative 10; Mismatches 27; Indels
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REFERENCE/DOCKET NUMBER: 325800-317
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08459101A
Patent No. 5945300
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LENGTH: 374 AMINO ACIDS
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: FROTEIN
MOLECULE TYPE: PROTEIN
US-08-468-847B-12
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US-08-459-101A-2
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APPLICANT: SCHOLLS, STAIN
APPLICANT: ALLEN, MATGATEL
APPLICANT: SVERDRUP, Fran
APPLICANT: CARMICHAEL, Bran
APPLICANT: CARMICHAEL, BRAN
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF UN
FILE REFERENCE: FIBROLIOO-1
CURRENT PELLING DATE: 1999-04-14
PRIOR PLILING DATE: 1999-04-14
PRIOR PLILING DATE: 1999-04-14
PRIOR PLILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-10-6
NUMBER OF SEQ ID NOS: 18
SPIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SCOTUM SAFETIMENT OF SEQ ID NOS: 18
CSCOTUM SAFETIMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 KOLNEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFOPNC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 KHOCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEFWVCDEDSIKDSLDDQDD 177
                                                                                                                                                                                                  61 QLGELCTERDPCDPHKGLFCDFGSPANRKIGVCPAK-DGAPCVFGGSVXRSGESFQSSCK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 SKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLXKGKKCSKTKKSPEPVRFT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 QINEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCK 118
                                                                                                                                                                                                                                                                           119 HQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                168 ------RDRTVVGPALAAYRIEDTFGPDFTWM-----RANCLVQTTEWSAC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 YAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNC 357
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                                                                                                                                                                                                                                                                                                                                                                                179 LGLDASEVELTRNNELLAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGOKCIVQTTSWSQC
                                                                                                             1 MLASVAGPVSLALVLILCTRPATGQDCSAQCQCAREAAPRCPAGVSLVLDGCGCCRVCAK
                                                             1 MSSSTFRTLAVAVTLLHLTRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCAK
                                                                                                                                                                                                                                                                                                               120 YQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRRVKLPGKCCESWVCDEP-----
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              38;
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              61; Mismatches 104; Indels
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45.5%; Score 957.5; DB 4;
Best Local Similarity 46.8%; Pred. No. 3.4e-73;
Matches 178; Conservative 60; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | |: || : | | SEGDNDIFESLYYRKMYGDM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09292036; Patent No. 6358741; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHPNEASFRLY -- SLFNDI 374
              Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-09-292-036-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 SVKKYRPKYCGSCVDGRCCTPQQTRTVKIRFRCDDGETFTKSVMMIQSCRCNYNCPHANE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 PCDHTKGLECNFGASPAATNGICRAQSEGRPCEYNSKIYQNGESFQPNCKHQCTCIDGAV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 EVELTRNNELIAIGKGSSLKRLPVFGTEP--RVLFNPLHAHGQKCIVQTTSWSQCSKSCG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCIFLCPOELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL----LGLDAS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 ALAAALICLARLALGSPCPAVCQCPAAAPQCAPGVGLVPDGCGCCKVCAKQLNEDCSRTQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AVAVTLLHLTRLAL-STCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.3%; Score 1646.5; DB 1; Best Local Similarity 80.1%; Pred. No. 2e-131; Matches 302; Conservative 22; Mismatches 36;
NAME: MULLINS, C.C. REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-442
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR EGO ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 ASFRLYSLFNDIHKFRD 379
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                                                                                                                                                                                                                                                                        STRANDEDNESS:
7 TOPOLOGY: LINBAR
WOLECULE TYPE: PROTEIN
US-08-468-8478-13
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Best Local Similarity
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; ORGANISM: Rat
US-09-582-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-582-337-2
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us-09-495-448a-2.rai

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268 BLSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKNAMFIKTCACHYN 327
118 KHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDD 177
                                                                                                                              ------KDRTÅVĞPALAAYRİBDTFĞPDPTMM-----RANCLVQTTBWSA 207
                                                                                                                                                                            237 CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296
                                                                                                                                                                                                                                                                  297 TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKWRFRCEDGEMFSKNVMMIQSCKCNYN 356
                                                                                                                                                                                                        208 CSKTCGMGISTRVTNDNTFCRLEKOSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPVKF
                                                                                   LLGLDASEVELTRNNELLAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
                       120 KYQCTCLDGAVGCVPLCSMDVRLPSPDCPPPRRVKLPGKCCKEWVCDEP----
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STATE: Illinois
CONDTRY: United States of America
CONDTRY: United States of America
ZIP: 66060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CIASSIPICATION: CADA-1999
CIASSIPICATION: CADA-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
OTHER INFORMATION: "Fisp12 amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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.larity 46.6%; Pred. No. 7.5e-73;
Conservative 61; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELETHONE: 312/474-6300:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERAX: 312/474-0448
   TTELEX: 25-3866
   INFORMATION FOR SEQ ID NO: 6:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 348 amino acids
   TYPE: amino acids
   STRANDEDNESS: single
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Patent No. 6413735
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Best Local Similarity
Matches 177; Conserva
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LIGIDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ 236
                                                                                                                                                                         297 TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN 356
                                                                                                                                                                                                        268 BLSGCTSVKTYRAKFCGVCTDGRCCTPHRITTLPVEFKCPDGEIMKKNNMFIKTCACHYN 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 KOLNEDCSKTOPCDHTKGLECNFGASSTALKGICRAOSEGRPCEYNSRIYONGESFOPNC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------KDRTAVGPALAAYRLEDTFGPDPTMM------RANCLVQTTBWSA 207
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                                                                                   237 CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSSSTPRTLAVAVTLIHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
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Sequence 15, Application US/08468847B
Sequence 15, Application US/08468847B
Sequence 15, Application US/08468847B
GENERAL INFORMATION:
TITLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CACCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: 16 BECKER FARM ROAD
STATE: 16 DECKER FARM ROAD
STATE: 10 0008
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45.3%; Score 953.5; DB 1;
Best Local Similarity 46.6%; Pred. No. 7.5e-73;
Matches 177; Conservative 61; Mismatches 103;
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REGISTRATION NUMBER: 33,073
REPERENCE/DOCKET NUMBER: 325800-442
TELECOMMINICATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/468,847B
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 348 AMINO ACID
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
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                                                                                                                                                         113 FORNCKHOCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGOCCEEWVCDEDSIKDSL 172
                                                                                                                                                                                                                                                                                                                      232 TSWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSP 291
                                      29
                       53 CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES
                                                                                                      204 TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCWVRPCBADLEENIKKGKKCIRTPKIS
                                                                                                                                                                                                                                                                                                                                                                                                  292 BPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSC
1 MSSSTRRILAVAVTLIALTRIALSTCPAA-----CHCPLE-APKCAPGVGLVRDGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,680
FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 KCNYNCPHPNEASFRLY -- SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 ACHYNCPGDNDIFESLYYRKMYGDM 348
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REPERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-FBB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
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APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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US-08-386-680-2
; Sequence 2, Application US/08386680
; Patent No. 5585270
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STATE: CA
COUNTRY:
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                                            237 CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296
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                                                                                                                                                                                                                                                                                                                                                                  KOLNEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNC 117
                                                                                               KHOCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCBEWVCDBDSIKDSLDDQDD 177
                                                                                                                       178 LLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
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45.2%; Score 950; DB 1; Length 349;
Best Local Similarity 45.7%; Pred. No. 1.5e-72;
Matches 176; Conservative 64; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Cortendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Inbitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIF: 92037

COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
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JULESSE: Spensley Horn Jubas & Inbitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
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CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Ur. Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECHONE: 619-455-5100
TELEFAX: 619-455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                        CPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                               328 CPGDNDIFESLYYRKWYGDM 347
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US-08-167-658-2
Sequence 2, Application US/08167628
Patent No. 5408040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-167-628-2
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92037
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352 KCNYNCPHPNEASFRLY -- SLFNDI 374
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NAME: Wetherall, 'Ur. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/752,427
             MOLECULE TYPE: protein US-08-459-717-2
linear
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STATE: CO
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                                                          Gaps
                                                             48;
                 45.2%; Score 950; DB 1; Length 349;
45.7%; Pred. No. 1.5e-72;
ive 64; Mismatches 97; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 02-UN-1995
CLASSIPICATION: 536
PRIOR APPLICATION: 536
PROR APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: Wetherell, '1r Ph.D., John W.
REGISTRALION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
MATTORNEY CARE, NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
MOTORIAND CARE, NUMBER: PD-1294
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Patent No. 5770209

GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUNESSEE: Spensley Horn Jubas & Lubitz STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA COUNTY: CA
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                                       Best Local Similarity 45.7
Matches 176; Conservative
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                                                                                              1 MSSSTFRTLAVAVTLIHLTRLALSTCPAA-----CHCPLE-APKCAPGVGLVRDGCGC
                                               Gaps
                                               48;
Length 349;
Query Match
Best Local Similarity 45.7%; Pred. No. 1.5e-72;
Matches 176; Conservative 64; Mismatches 97; Indels
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Patent No. 5783187
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gretendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11.58P-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 14225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
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Best Local Similarity 45.7%; Pred. No. 1.5e-72;
Matches 176; Conservative 64; Mismatches 97; Indels 48; Gaps
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEPAX: 619-455-5100
TELEPAX: 619-455-5100
SEQUENCE CHARATERISTICS:
LENGTH: 349 amino acids
TYPE: amino acids
TYPE: amino acid
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TYPE: amino acids
US-08-712-302-2
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Search completed: April 22, 2004, 18:00:05 Job time : 17.4566 secs

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AAR25565 standard, protein, 379 AA.
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ID AAR?
                                                                                                            April 22, 2004, 17:51:09; Search time 49.8684 Seconds (without alignments) 2147.361 Million cell updates/sec
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2103
1 MSSSTFRTLAVAVTLIHLTR......PNEASFRLYSLFNDIHKFRD 379
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                 1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2002s:*
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geneseqp2004s:*
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

The protein sequence was deduced from the DNA sequence obtd. by screening a cDNA library made from AKR-2B mouse cells induced with TGF-betal and grotochexamide with two probes from untreated AKR-2B mRNA and AKR-2B mRNA from cells treated with cyclohexamide and TGF- betal. The proteins encoded by hybridising colonies (beta-IG-M1 and beta-IG-M2) contain 38 cys residues and are induced by TGF-betal. Beta-IG-M2 displays 80 percent homology to the CEF-10 protein induced by v-src in chicken embryofibroblasts and is identical to the protein encoded by cyrel, an immediate early response gene induced in quiescent BALB 3T3 cells by immediate early response gene induced in quiescent BALB 3T3 cells by serum treatment. Residues 49-56 of beta-IG-M1 conform to the GCGCCXC motif reported in the amino half of insulin-like growth factor (IGF) growth factor beta; induced; CEF-10; v-src; chicken; embryo; TGF-beta. TGF-beta induced gene family - encodes proteins involved in growth and differentiation effects of TGF-beta-1. Chinn J, Neubauer MG; (BRIM) BRISTOL-MYERS SQUIBB CO. Claim 2; Fig 1; 35pp; English. 91US-00642991. 92US-00816270. 92EP-00300429. (revised)
(first entry) Purchio AF, Brunner AM, WPI; 1992-243508/30. N-PSDB; AAQ26421. Transforming fibroblasts; 18-JAN-1991; 10-JAN-1992; 17-JAN-1992; Mus musculus EP495674-A2 25-MAR-2003 18-JAN-1993 22-JUL-1992 Beta-IG-M1

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Cyr61 protein
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binding proteins. The C-terminal Cys rich region of beta-IG-Mi, -M2 and CEF-10 contain an amino acid sequence with strong homology to a motif found near the C-terminal of the malarial circumsporozoite (CS) protein, which is highly conserved among all species of malarial parasites stequenced to date (designated region II). This motif is also found in other proteins which have cell adhesive properties that mediate cell-cell and cell-extracellular matrix interactions, such as propertin, thrombospondin, and TRAP. The proteins encoded by TGF-beta induced genes are likely to be involved in mediation of the biological effects of TGF-beta relating to cell growth and differentiation. See also AAR25566. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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                                                                                                                                                             100.0%; Score 2103; DB 2;
100.0%; Pred. No. 2.7e-155;
cive 0; Mismatches 0;
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The invention relates to extracellular matrix (ECM) signalling molecules involved in cellular response to growth factors. More particularly the involved in cellular response to growth factors. More particularly the involved in directed to cysteine-rich protein (Cyrel), and connective rissue such as fibroblast secreted protein (Fright2) and connective rissue growth factor (CTGF) and nucleic acid molecules encoding such proteins. The polypeptides of the invention are members of cysteine-rich secreted protein family. Human Cyrel fragment is useful in methods for screening modulators of cell adhesion, cell migration, fibroblast cell confiferation, angiogenesis, wound healing and Cyrel-integrin receptor interaction. Modulator of Cyrel-integrin alphavbeta3 interaction is used for the preparation of a medicament for the treatment of atherosclerosis, heart disease, tumour metastasis, fibrosis, tumour growth, disorders associated with inadequate angiogenesis; aberrant granulation tissue development; abstrant fibroblast growth and wounds. Polymucleotides of the invention are useful in gene therapy. The present sequence is mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human cysteine-rich protein 61 (Cyr61) fragment useful in for screening for modulators of cell adhesion, fibroblast cell proliferation, angiogenesis and cell migration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 1; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEASFRLYSLFNDIHKFRD 379
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                                                                31-JAN-2000; 2000US-00495448.
15-MAY-2000; 2000US-0204364P.
06-OCT-2000; 2000US-0238705P.
31-JAN-2001; 2001WO-US003267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100. Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465561/50.
N-PSDB; AAD11220.
                                                                                                                                                                                                                 (MUNI-) MUNIN CORP.
                                                                                                                                                                                                                                                                                     Yeung C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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    CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
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                            301 CSSVKKYRPKYGGSCVDGRCCTPLQTRTVROMFRCEDGEMFSKNVMMIQSCKCNYNCPHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NEDCSKTQPCDHTKGLECNPGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CICIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSSRIARALALVVTLLHITTRIALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 --LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A monocyte mature differentiation factor - useful for the long term tissue culture of macrophage(s).
                                                                                                                                                                                                                                                                                                                                                                                       monocyte; mature; differentiation factor; MMDF; macrophage;
immune activator; tissue culture; infectious disease.
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                                                                                                                                                                                                                                                                                                                                              Human monocyte mature differentiation factor.
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                                                                                                                                                                                                                            Ş
                                                                                  361 NEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                          AAW35957 standard; protein; 381
                                                                                                                  361 NEASFRLYSLFNDIHKFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                       05-MAR-1998
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                                                                                                                                                                                                                                                              AAW35957;
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    301
                                                                                                                                                                                                                                                                                                                                                                                                               cancer;
                                                                                                                                                                                                                                                                                                                                                                                          Human:
                                                                                                                                                                                   RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCGF). SCGF has vulnerary and osteopathic activities, and can be used in gene therapy. The SCGF polypeptides and polynucleotides can be used for treating muscle wasting diseases, and osteoporosis, and to stimulate wound healing and tissue regeneration, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CNN family protein which is given in comparison with the human SCGF in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCREWVCDEDSIKDSLDDQDDLLG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polynucleotide sequence encoding a human small CCN-like growth factor, useful for treating muscle wasting disease, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSSSTFRTLAVAVTLHTTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                              Human; small CCN-like growth factor; SCGF; vulnerary; osteopathic; gene therapy; muscle wasting disease; osteoporosis; wound healing; tissue regeneration; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes human small CCN-like growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indela
                                                                                                                                          Mouse cyr6 CNN family protein sequence SEQ ID NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2103; DB 5;
100.0%; Pred. No. 2.7e-155;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2A-D; 33pp; English.
                   ABB09201 standard; protein; 379 AA
                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-2001; 2001US-00853625.
                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00468847.
                                                                                                 (first entry)
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Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAST/) HASTINGS G A. (ADAM/) ADAMS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-382150/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
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                                                                                                                                                                                                                                                                                                     US2002049304-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hastings GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                   08-JUL-2002
                                                                                                                                                                                                                                                                                                                                              25-APR-2002
                                                            ABB09201;
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TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRIVKARFRCEDGETFSKNVAMIQSCKCNYN 358
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KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--OGOKCIVOTTSWSO
                                                                          239 CSKTCGTGISTRVTNDNPBCRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                                                                                                          TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, uterine leiomyoma proliferation, uterine leiomyoma formation, Cyr61; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or inhibiting proliferation
s modulating or increasing th
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llarity 91.4%; Pred. No. 1.9e-142;
Conservative 9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu Y, Winneker R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preventing uterine leiomyoma formation o uterine leiomyoma in subject, comprises level of Cyr61 in leiomyoma tissue.
                                                                                                                                                                                                                                      CPHPNEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                    ||| || || || || CPHANEAAFPFYRLFNDIHKFRD 381
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                                                                                                                                                                                                                                                                                                                                                                                                       AAU79761 standard; protein; 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Cyr61 protein.
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Best Local Simi
Matches 350;
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                    TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKWRFRCEDGEMFSKWWMIQSCKCNYN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shear stress-response protein; vascular disease; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
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                                                     TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMIQSCKCNVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawabata A, Sakurada K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences, proteins encoded by them and antibodies against useful in diagnosis and treatment of vascular disease caused by arteriosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human shear stress-response protein SEQ ID NO: 46.
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ilarity 91.4%; Pred. No. 1.9e-142;
Conservative 9; Mismatches 18;
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Sugano S;
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                                                                                                                CPHPNEASFRLYSLFNDIHKFRD 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK. (NOJI/) NOJIMA H.
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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T. Sekine S,
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N-PSDB; AAH02896.
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Best Local Similarity
Matches 350; Conserv
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Kuga T,
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cell proliferation by blocking sex steroid induced and growth factor is epidermal, heparin binding epidermal or basic fibroblastic growth factor. (I) can be used to diagnose or stage breast cancer where the level of Cyr61 in a positive/suspect breast cancer where the level of Cyr61 in a positive/suspect breast cancer cell is compared to the level in a normal tissue indicates the presence of breast cancer. The level of Cyr61 being determined by exposing the tissues to (I), and an increase in the level of bound antibody by the suspect/positive cell as compared to the normal tissue indicates the presence of breast cancer. The present sequence represents the human Cyr61 protein, which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, angiogenesis, connective tissue growth factor-2; CTGF-2; tumour; ischaemia; restenosis; tissue repair; wound healing; congenital defect; cardiovascular disease, atherosclerosis; heart failure; angina; trauma; burns; osteoporosis; periodontal disease; liver failure; tranquillizer; vulnerary; cosmetic plastic surgery; vasotropic; hepatotropic; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTISWSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                              CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL--
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Best Local Similarity 91.4%; Pred. No. 1.9e-142;
Matches 350; Conservative 9; Mismatches 18;
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47. .51
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                                                                                                             CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL-- 178
                                                                                                                                                                                                                                                                                                                    The present invention describes a method for the prevention or inhibition of breast cancer cell proliferation. The method comprises administration of a compound that inhibits the interaction of a sex steroid receptor with a sex steroid response element of the Cyfol (cysteine rich heparinbinding protein) promoter. Cyfol has cytostatic activity, An antibody (I) which neutralises Cyfol can be used to prevent or inhibit breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regulation of Cyr61 expression and activity for preventing and inhibiting breast cancer comprises use of a Cyr61 neutralizing antibody, an antisense oligonucleotide and an antibody which.
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NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                           KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ
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                                                                                                                                                                        --LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGOKCIVQTTSWSQ
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                                                                                                                                                                                                                                                                                                                                                                                   Human Cyr61 protein SEQ ID NO:2.
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16-MAY-2001; 2001US-0291510P.
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N-PSDB; ABA93127, ABA93130.
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236 238

CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180

121 121 179

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1 MSSRIARALALVVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60

NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSR1YQNGESFQPNCKHQ CTCIDGAVGCIPLCPQELSIPNIGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL-- CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296

237 239 297 299 357

CSKICGIGISIRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKIKKSPEPVRF

181 KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ

-- LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ

TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMNIQSCKCNYN 358

CPHPNEASFRLYSLFNDIHKFRD 379 CPHANEAAFPFYRLFNDIHKFRD 381

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TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN 356

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The present invention relates to a method for stimulating angiogenesis in a mammal. The method comprises administering a polynucleotide encoding connective tissue growth factor-2 (CTGP-2) or an active fragment or its connective. The method is useful for stimulating angiogenesis in a mammal preferably human having is useful for stimulating angiogenesis in a mammal revascularisation which is leg or arm. The invention is useful for limbiting tumour growth, where angiogenesis is utilised for enhancing the repair of connective and support tissue, promoting the attachment, fixation and stabilisation of tissue implants and enhancing wound haling, hence is useful for treating cardiovascular disease e.g. atherosale rosis, reperfusion injury such as heart failure, angina, is chaemia; and is also used to differentiate, proliferate and attract cells leading to regeneration of tissues which is utilised to repair corporate tissue damaged by congenital defects, trauma (burns, ulcer, etc) age, disease (e.g. osteoporosis, periodontal disease, liver failure), surgery including cosmetic plastic surgery. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimulating angiogenesis in a mammal preferably human having ischemia restenosis or is treated for limb revascularization, by administering connective tissue growth factor-2 polypeptide or polynucleotide.
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                                                        "Immunogenic epitope"
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337. .343
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"Immunogenic epitope'
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                                                                     164. .176
/note= "Immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2001; 2001WO-US021799
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18-MAY-2001; 2001US-0291642P
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244
/note= "T-
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/note= "T-
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/note= "Im
223. .228
/note= "Im
239. .244
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/note= "Im
279. .296
                                         .150
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N-PSDB; AAD29095.
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Human, connective tissue growth factor 2, CTGF-2, support tissue, tissue repair, skin disorder, injury, acne, UV damage, burn, wrinkled skin, tissue implant, vulnerary, antiaging, dermatological, antiseborrhoeic.

94WO-US007736. 95US-00459101. 99US-00348815

US6534630-B1. Homo sapiens

08-JUL-1999; 12-JUL-1994; 02-JUN-1995;

18-MAR-2003

(HUMA-) HUMAN GENOME SCI INC

Human connective tissue growth factor 2 (CTGF-2) #1.

17-OCT-2003 (first entry)

ABU63222;

ABU63222 standard; protein; 381 AA

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Claim 1; Col 23-24; 20pp; English.
                                                                       or burns, and wrinkled skin.
                                                           WPI; 2003-553676/52.
N-PSDB; ACD26170.
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Gaps 9

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MSSSTPRILAVAVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKOL

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The present invention relates to the isolation of human connective tissue growth factor 2 (CTGF-2), and the polyuncleotide sequence encoding it. The CTGF-2 polypeptide is useful for enhancing the repair of connective and support tissues, for treating skin disorders such as injuries, acne, UV damage or burns, and wrinkled skin, for promoting attachment, fixation and stabilisation of tissue implants, and as an immunogen to produce
                                                                                                                                                                                                                                                              New human connective tissue growth factor 2 polypeptides and polynucleotides useful for enhancing repair of connective and support tissues, and for treating skin disorders, e.g. injuries, acne, UV damage
     Adams MD;
Li H,
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99US-0124270P

12-MAR-1999;

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NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
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                                                                                                                                                                                                                                                                                                                           antibodies. The polynucleotide sequence encoding CTGF-2 may be used as a hybridisation probe for a cDNA library to isolate the full-length cDNA and other cDNAs, which have high sequence similarity to the CTGF-2 gene or similar biological activity. The polynucleotides are also useful for producing polypeptides by recombinant techniques, and in chromosome identification. The present sequence represents human CTGF-2. Note: The present sequence given as SEQ ID No:2 in the sequence listing differs from that given in Fig 1 (ABU63223)
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                                                                                                                                                                                                                                                                                                  1 MSSSTERTLAVAVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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                                                                                                                                                                                 Sequence 381 AA;
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AAC77607 to AAC78448 encode the human cancer associated proteins given in the tissues and calls the genes are expressed in. Example of activities tissues and calls the genes are expressed in. Example of activities include: cytocratic; proliferative; vulnerary; immunomodulator; antidabetic; antiathmatic; antitheumatic; antiathratic; antidathratic; antidabetic; antiathmatic; antitheumatic; antidabetic; antidathratic; antidation or mobilisation of inmune cells, to treat disorders and antagonists from the proliferation, differentiation or mobilisation of immune cells, to treat disorders and organ rejection, modulate haemostatic or thromolytic activity, modulate (inflammation, cancers, cardiovascular disorders, neurological disease and antagonists may be also be used in drug sorreens. AAC78457 and AAB44240 represent sequences used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may be also be used in the exemplification of antagonists may antagonists may antagonist
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                                                                                                                                                                                                                                   acids comprising sequences encoding peptides diagnosing e.g. cancer.
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Best Local Similarity 91.4%; Pred. No. 2.3e-142;
Matches 350; Conservative 9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                  Claim 11; Page 2116-2118; 2352pp; English.
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                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                      solated nucleic for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention
                                                                                                                                                       2000-587533/55
                                                                                                                                                                                 N-PSDB; AAC78196
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                                                                                                        Rosen CA,
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RESULT 11 ABG76937

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The invention discloses the isolated human polypeptides, and polymucleotides encoding them, that have been designated SECX and NOVX. The polymucleotides can be used for treating, or delaying, the onset of an engiogenic-associated disorder or treating a pathological state in a sugiogenic-associated disorder or treating a pathological state in a subject, preferably a mammal. They can also be used in determining the presence of, or predafaposition to, a disease associated with altered levels of the polypeptides and polymucleotides of any one of the 12 sequences (SEC1-12), for raising antibodies, for identifying an agent that modulates the expression or activity of the polypeptide, or treating or preventing a NONX-associated disorder (NOV1-8) and as a pharmaceutical composition comprising the polypeptide, or treating or preventing a mounts are assessed, or for the manufacture of a medicament (e.g. gene therapy) for treating or preventing disorders or syndromes such as developmental disorders, immune diseases, singual transduction pathway disorders, metabolic disorders, neurodegenerative disorders (including Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SECX/NOVX polypeptide useful for diagnosing, preventing or treating disorders associated with aberrant expression or activity of SECX/NOVX nucleic acids and proteins e.g., diabetes.
                                                                                                                                                     Human; SEC; NOV; immunosuppressive; hepatotropic; antiinflammatory; angiogenic-associated disorder; diagnostic; gene therapy; developmental disorder; immune disease; signal transduction pathway disorder; metabolic disorder; feeding disorder; obesity; watting disorder; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; behavioural disorder; asthma; atherosclerosis; cardiomyopathy; angina pectoris; autoimmune disease; retinal disease; cirrhosis; diabetes; infectious disease; unan immunodeficiency virus; Huy; cancer; hypertension; hypertension; multiple sclerosis; utinary retention; osteoporosis; crohn's disease; ulcer; neurological disorder; anxiety;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rastelli L, Herrmann JL, Macdougall JR, Zhong H;
Boldog F, Shimkets RA, Gorman L, Crasta OR, Mysore KK,
Martin GB, Eisen A, Spaderna SK, Vernet CAM, Bergh C;
Dipippo VA, Zerhusen BD, Peyman JA, Ellerman K, Stone
Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
                                                                                                                         comprising CYR61, designated SEC1.
                                                                                                                                                                                                                                                                                                                                                                                             haemophilia; cirrhosis; immunogen; vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 9; 443pp; English
ABG76937 standard; protein; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-2001; 2001US-0261013P.
11-JAN-2001; 2001US-0261014P.
11-JAN-2001; 2001US-0261018P.
11-JAN-2001; 2001US-0261028P.
11-JAN-2001; 2001US-0261028P.
17-AUG-2001; 2001US-0313170P.
10-SEP-2001; 2001US-0318410P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2002; 2002WO-US000609
                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
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N-PSDB; ABS59522
                                                                                                                           Human protein,
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Folkerts O,
Spytek KA, D
Grosse WM, A
Edinger S;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                               05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JJL-2002
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TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKARPRCEDGETFSKAVMAIQSCKCNYN 358
                                                                                                     They may
parkinson's disease), behavioural disorders, allergies, asthma, atherosclerosis, cardiomyopathy, angina pectoris, autoimmune diseases, retinal disease, cirrhosis, diabetes, infectious disease (bacterial, fungal, protozoal and viral e.g. human immunodeficiancy virus, HIV), cancer (e.g. prostate cancer), hypertension, hypotension, multiple sclerosis, uninary retention, osteoporosis, (rohm's disease, ulcers, neurological disorders (e.g. anxiety), haemophilia or cirrhosis. They malso be used as immunogens to produce antibodies specific for the invention, and as vaccines. Further, they are useful for screening potential agonist and antagonist compounds. The sequences presented in ABG76937-ABG76956 are the human SEC1-12 and NOV1-8 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSKTCGTGISTRVTNDNPECRLVKGTRICEVRPCGQPVYSSLKKGKKCSKTKKSPBPVRF
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                                                                                                                                                                                                                               91.8%; Score 1930; DB 5;
90.9%; Pred. No. 7.9e-142;
cive 10; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPHPNEASFRLYSLFNDIHKFRD 379
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2001US-0314356P.
2001US-0325020P.
2001US-0341746P.
2002US-0362158P.
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.9°
Matches 348; Conservative
                                                                                                                                                                                                     Sequence 381 AA;
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25-SEP-2001;
12-DEC-2001;
05-MAR-2002;
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a OR, Mysore KK;
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238 296

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Claim 2; Page 112-113; 133pp; English.
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N-PSDB; AAT94699.
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hes 348; Conserv
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modulate e.g. hae
regeneration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 381 AA;
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                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                            the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer. The method prostate cancer by comparing the level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in a level of expression of the marker in a level indicates that the patient is afflicted with prostate cancer. Nucleic eacles of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB7517-ADB7531 represent marker cNNA and proteins. Note: The sequence data for this patent did not form pat of the printed specification, but the wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVGMRFRCEDGETFSKNVMMIQSCKCNYN 358
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                                                                                                                                                    The invention relates to newly discovered cancer markers associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- LGLDASEVELTRNNELLAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSKTCGTG1STRVTNDNPECRLVKETR1CEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN
                                                                                        nucleic acid molecule, useful for diagnosing or treating prostate
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                          Gorbatcheva
Anderson D;
                                                                                                                                                                                                                                                                                                                                                                                                        ? 9
                                                                                                                                                                                                                                                                                                                                                                               Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                          Endege WO, Gannavarapu M,
nsey AM, Glatt K, Zhao X,
                                                                                                                                                                                                                                                                                                                                                                               91.8%; Score 1930; DB 7; 90.9%; Pred. No. 7.9e-142; ive 10; Mismatches 19;
                                                                                                                           Disclosure; SEQ ID NO 84; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cysteine rich protein 61 (Cyr61)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPHPNEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPHANEAAFPFYRLFNDIHKFRD 381
              Monahan JE, Endest
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(MILL-) MILLENNIUM PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                        Kamatkar S,
                                                              WPI; 2003-248033/24
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 348; Conserv
                                                                                                                                                                                                                                                                                                                                                        Sequence 381 AA;
                          Schlegel R,
                                        Hoersh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This protein sequence comprises human cysteine rich protein 61 (Cyr61), an extracellular matrix signalling molecule. Its amino acid sequence was deduced from a human placental cDNA clone (see AAP94699). Cyr61 bolypeptides can be expressed in transformed or transfected host cells. Cyr61 can be used to modulate haematostasis, induce wound healing in a tissue, promote organ regeneration, improve tissue grafting or promote bone or prothesis implantation (claimed). Ic can also be used to screen for a modulator of angiogenesis, chondrogenesis, oncogenesis, cell adhesion, cell migration, cell proliferation, expand a population of undifferentiated haematopoietic stem cells in culture and to screen for a mitogen (claimed). Ex vivo methods for using mammalian extracellular matrix signalling molecules to prepare blood products are also provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
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                                         cell migration;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGOKCIVQTTSWSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and purified cysteine rich protein 61, Cyr61 - useful tc e.g. haematostasis, induce wound healing, promote organ
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Cysteine rich protein 61; Cyr61; human; extracellular matrix signalling molecule; cell adhesion; cell recell proliferation; angiogenesis; chondrogenesis; oncogenesis; haematostasis; wound healing; organ regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 381;
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larity 90.9%; Pred. No. 9.4e-142;
Conservative 10; Mismatches 19;
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involved in cellular response to growth factors. More particularly the invention is directed to cysteine-rich protein (Cyfsi), and Cyfsi-related proteins such as fibroblast secreted protein (Fispl2) and connective tissue growth factor (CTGF) and mucleic acid molecules encoding such secreted proteins. The polypeptides of the invention are members of cysteine-rich secreted protein family. Human Cyfsi fragment is useful in methods for screening modulators of cell adhesion, cell migration, fibroblast cell proliferation, angiogenesis, wound healing and Cyfsi-integrin receptor interaction is used for the preparation of a medicament for the treatment of atherosciencial sesciated with inadequate angiogenesis, tumour growth, disorders associated with inadequate angiogenesis; aberrant granulation tissue development; aberrant fibroblast growth and wounds. Polynucleotides of the invention are useful in gene therapy. The present sequence is human
                                                                                                                                                                                                                     Cysteine-rich protein, Cyr61; extracellular matrix signalling molecule; fibroblast secreted protein; Fisp12; connective tissue growth factor; CTGF, ECM; cell adhesion; cell migration; fibroblast cell proliferation; angiogenesis; wound healing; integrin receptor; atherosclerosis; tumour; heart disease; fibrosis; gene therapy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to extracellular matrix (ECM) signalling molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human cysteine-rich protein 61 (Cyr61) fragment useful in methods for screening for modulators of cell adhesion, fibroblast cell proliferation, anglogenesis and cell migration.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
163. .229
/note= "Cysteine free region"
212. .281
/note= "Domain III"
282. .381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 30; Page 171-172; 186pp; English.
 CPHANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                                                                        Human cysteine-rich protein (Cyr61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Domain IV"
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                                                                                  AAE05921 standard; protein; 381
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15-MAY-2000; 2000US-0204364P.
06-OCT-2000; 2000US-0238705P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2001; 2001WO-US003267
                                                                                                                                                     (first entry
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Best Local Similarity
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                                                                                                                     AAE05921;
 359
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                                                                                                                                                                                                                                                                                                                                                               Key
Region
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                                                   RESULT 14
                                                                     AAE05921
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Length 381;

Score 1929; DB 4; Pred. No. 9.4e-142;

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CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF 296
                                                                                                                                                                                                                                                                 TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYN 356
                                                                                                                                                                                                                                                                                      TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMIQSCKCNYN 358
                                                                    61 NEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNCKHO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human small CCN-like growth factor (SCGF). SCGF has vulnerary and osteopathic activities, and can be used gene therapy. The SCGF polypeptides and polymucleotides can be used for treating muscle wasting diseases, and osteoporosis, and to stimulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated polynucleotide sequence encoding a human small CCN-like growth factor, useful for treating muscle wasting disease, and
                                      61 NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCQHQ
                                                                                                                                                                                                                                 --LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
                        1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, small CCN-like growth factor; SCGF; vulnerary; osteopathic; gene therapy; muscle wasting disease; osteoporosis; wound healing; tissue regeneration; anglogenesis.
9
Indels
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCGF CNN family protein sequence SEQ ID NO:12.
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2A-D; 33pp; English.
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10,
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002049304-A1.
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01-APR-1998;
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 348;
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                                                                                                                                                                                                                                                                                                                                                               239 QCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKGSPEPVR 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 FIYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRIVKARFPCEDGETFSKAVAMIQSSKCNY 358
                                                                                                                                                                                                                                                                                                                                              CTCIDGAVG-CIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL- 178
                                                                                                                                                                                                                                                                                                                                                                                                                179 --- LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGOKCIVQTTSWS 235
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                                                                                                                                                                                                         1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
                                                                                                                                                                                                                             wound healing and tissue regeneration, to promote angiogenesis and to stimulate proliferation of vascular smooth muscle and endothelial cell production. The present sequence represents a CNN family protein which given in comparison with the human SCGF in the exemplification of the present invention
                                                                                                                                                                          Gaps
                                                                                                                                                                          7.
                                                                                                                                   86.5%; Score 1819.5; DB 5; Length 374; 88.3%; Pred. No. 3e-133; ive 10; Mismatches 27; Indels 7;
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Best Local Similarity 88.3:
Matches 332; Conservative
                                                                                                    Sequence 374 AA;
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Search completed: April 22, 2004, 17:56:32 Job time : 52.8684 secs

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US-09-853-625B-11
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                                                                                                                                                                                      April 22, 2004, 17:58:40 ; Search time 38.3987 Seconds (without alignments) 2728.846 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                        US-09-495-448A-2
2103
1 MSSSTFRTLAVAVTLAHLTR......PNEASFRLYSLFNDIHKFRD 379
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PC7_NBW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NBW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_WUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_WUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_WUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                  OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 11, Appl	Sequence 2, Appli	Sequence 45, Appl	Sequence 2, Appli	Sequence 45, Appl	Sequence 60, Appl	Sequence 62, Appl	Sequence 44, Appl	•	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 42, Appl		Sequence 2, Appli
QI	US-09-853-625B-11	US-10-053-753-2	US-10-099-322-45	US-10-182-432-2	US-10-044-564-45	US-10-464-368-60	US-10-464-368-62	US-10-099-322-44	US-10-044-564-44	US-09-901-910-2	US-10-294-796-2	US-10-394-015-5	US-10-099-322-42	US-10-044-564-42	US-10-381-644-2
90	ָּה	13	12	15	15	16	16	15	15	10	14	14	15	15	16
% Query Match Length DB	379	379	379	379	379	379	379	381	381	381	381	381	381	381	381
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	98.7	92.3	92.3	92.2	92.2	92.2	92.2	92.2	92.2
Score	2103	2103	2103	2103	2103	2103	2076	1942	1942	4938	1938	1938	1938	1938	1938
Result No.		N	٣	4	Ŋ	9	7	80	6	10	11	12	13	14	15

61	43	equence 43	43	equence 84	equence 2,	equence 41	equence 2,	equence 41	equence 4,	Sequence 4,		ŗ,	quence 13,	equence 63	equence 7,	equence 56	equence 2,		quence 15,	e e	equence 8,	ý	equence 54	equence 4,	26	æ	equence 17	eguence 46	Sequence 78, Appl	
0-464-368-6	-925-301-14	0-099-322-4	0-044-564-	0-205-823-8	0-099-32	0-099-322-	0-044-56	0-044-564-	0-053-753-	.0-182-432-	53-625B	19-901-910-	1-853-625B	.0-464-368-6	.0-245-977-	0-464-368-	0-390-98	.0-101-040-	9-853-625B-	10-053-753-	10-245-977-	-182-4	10-464-368	10-101-040-	10-011-859	10-053-753-	10-060-036-1	10-171-311	-10-205-823-7	
16	σ	15	12	14	15	15	15	15	13	15	σ	2	თ	16	14	16	14	13	σ	13	14	15	16	13	13	13	14	14	14	
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

US-09-853-625B-11

| Sequence 11, Application US/09853625B
| Patent No. US/0020049304A1
| CENERAL INFORMATION:
| PATENT HASTING: Haman CCN-Like Growth Factor TITLE OF INVENTION: HOMAN CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
| CORRESPONDENCE ADDRESS: 20
| CORRESPONDENCE ADDRESS: 20
| CORRESPONDENCE ADDRESS: 20
| CITY: ROSELAND STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY
| COUNTRY: USA COUNTRY: US

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CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
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                                                                                                                                      NAWE/KEY: misc feature

OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-053-753-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Microscinos al.
APPLICANT: Microscope al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same TITLE OP INVENTION: Proteins and Nucleic Acids Encoding Same CURRENT APPLICATION NUMBER: US/10/099,322
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2002-01-11
                                                                                                                                                                                                                                                                                                                                             Length 379
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                          ; Score 2103; DB 13;
; Pred. No. 1.8e-166;
0; Mismatches 0;
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US-10-099-322-45
US-10-099-322-45
Sequence 45, Application US/10099322
Publication No. US20030215449A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 379; Conservative 0
SEQUENCE CHARACTERISTICS
                                 LENGTH: 379 amino TYPE: amino acid
                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
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15-10-03-753-2
15-Sequence 2, Application US/10053753
15-Sequence 2, Application US/10053753
15-Sequence 2, Application No. US2002015098641
16-Sequence 2, Application No. US2002015098641
16-Sequence 2, Application No. US2002015098641
17-Sequence 2, Application Street F.
17-TILE OF INVENITION: Extracellular Matrix Signalling Molecules
17-Sequence ADDRESS:
17-Sequence ADDRESS:
17-Sequence ADDRESS:
18-September Solver Street Solver Narray & Borun STREET: Galo Sears Tower, 233 South Wacker Drive CTTY: Chicago STRATE: Illanois
17-Sequence America CONTRY: United States of America CONPUTER: END FO. Compatible CONFUTER: PATENTION: NUMBER: US/10/053,753
17-SERENCE/DOCKET NUMBER: 28758/33766
18-SERENCE/DOCKET NUMBE
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                                                                                                                                                                                                                    Query Match
100.0%; Score 2103; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.8e-166;
Matches 379; Conservative 0; Mismatches 0; Indels 0
STRANDEDNESS: «Unknown»
STRANDEDNESS: «Unknown»
STRANDEDNESS: «Unknown»
MOLECTLE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-853-625B-11
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LDASEVELTRANBELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGGKCIVQTTSNSQCSKS
                                                                CGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG
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WS-10-044-564-45

WS-10-044-564-45

WS-10-044-564-45

WS-10-044-564-45

Publication No. US20040018196A1

GENERAL INFORMATION:

APPLICANT Mezes et al.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same TITLE REFERENCE: 2140-2-40

FILE REFERENCE: 2140-2-40

CURRENT FILING DATE: 2001-09-09

PRIOR PPLICATION NUMBER: 60/261,018

PRIOR PPLICATION NUMBER: 60/261,018

PRIOR PLILING DATE: 2001-01-11

PRIOR PLILING DATE: 2001-03-10

PRIOR FILING DATE: 2001-03-10

PRIOR FILING DATE: 2001-01-11

PRIOR PLILIATION NUMBER: 60/261,026

PRIOR PLILING DATE: 2001-01-11

PRIOR PLILING DATE: 2001-03-11

PRIOR PLILIATION NUMBER: 60/213,170

PRIOR PLILIATION NUMBER: 60/313,170

PRIOR PLILIATION NUMBER: 60/313,170

PRIOR PLILIATION NUMBER: 60/313,170

PRIOR PLILIATION NUMBER: 2001-03-11

PRIOR PLILIATION NUMBER: 2001-03-11

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PRIOR PLILIATION NUMBER: 2001-03-11

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100.0%; Score 2103; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-166;
Matches 379; Conservative 0; Mismatches 0;
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Sequence 2, Application US/10182432

Sequence 2, Application US/10182431

Fublication No. US20040002124A1

GENERAL IMPORMATION:

APPLICANT: LAU Lester F., YEUNG, Cho-Yau, and GREENSPAN, Jeffrey A., TITLE OF INVENTION: CYR61 -COMPOSITIONS AND METHODS

FILE REFERENCE: 214448/00205

CURRENT APPLICATION NUMBER: US/10/182,432

CURRENT FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 379
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                                                                                                         Query Match
100.0%; Score 2103; DB 15; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.8e-166;
Matches 379; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-182-432-2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-099-322-45
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PRIOR APPLICATION NUMBER: 60/388,970
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patentin version 3.2
SEQ ID NO 62
LENTH: 379
TYPE: PRT.
TYPE: PRT.
US-10-464-368-62
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) Sequence 44, Application US/10099322
; Publication No. US20030215449A1
; GENERAL INFORMATION:
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Best Local Similarity 98.2%;
Matches 372; Conservative
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                                                                                                                                                                                   Sequence 60, Application US/10464368
Publication No. US20040023356A1
GENERAL INFORMATION:
APPLICANT: Krumlauf, Robb
APPLICANT: Ellies, Debra
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REPERENCE: 40716-IP-017
CURRENT FILING DATE: 2003-06-16
PRIOR PELLING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 60
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Publication No. US20040023356A1
GENERAL INFORMATION
APPLICANT: Krunlauf, Robb
APPLICANT: Ellies, Debra
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REFERENCE: 40716-1P-0105/464,368
CURRENT APPLICATION NUMBER: US/10/464,368
  CSSVKKYRPKYCGSCVDGRCCTPLQTRTVGARRCEDGEMPSKNVMIQSCKCNYNCPHP 360
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100.0%; Score 2103; DB 16; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.8e-166;
Matches 379; Conservative 0; Mismatches 0; Indels 0;
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                                                                                    NEASFRLYSLFNDIHKFRD 379
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CRGANISM: MOUSE
US-10-464-368-60
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APPLICANT: Wacses et al.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 2.402-340CIP
CURRENT APPLICATION NUMBER: 05/261,014
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR APPLICATION NUMBER: 60/261,013
PRIOR FILING DATE: 2001-01-11
       Length 379;
                                                                         Indels
Score 2076; DB 16;
Pred. No. 3.2e-164;
4; Mismatches 3;
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                                                  1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                      NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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          MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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| Bublication No. US20030012768A1
| GENERAL INFORMATION:
| APPLICANT: Li, Haddong
| APPLICANT: Calenda Valerie
| TITLE OF INVENTION: Connective Tissue Growth Factor-2
| TITLE OF INVENTION NUMBER: US/09/901,910
| CURRENT APPLICATION NUMBER: 09/348,815
| PRIOR APPLICATION NUMBER: 09/348,815
| PRIOR FILING DATE: 1995-00-08
| PRIOR FILING DATE: 1995-00-07-1
| PRIOR PRILING DATE: 2000-07-11
| PRIOR PRILING DATE: 2000-07-11
| PRIOR FILING DATE: 2000-07-11
| PRIOR FILING DATE: 2000-07-11
| PRIOR FILING DATE: 2001-07-11
| PRIOR FILING DATE: 2001-05-18
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: PatentIn Version 3.0
| SEG ID NO. 2
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Best Local Similarity 91.4%; Pred. No. 9.5e-153;
Matches 350; Conservative 9; Mismatches 18;
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ORGANISM: homo sapiens
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US-10-044-564-44

Sequence 44, Application US/10044564

Sequence 44, Application US/10044564

Publication No. US20040018196A1

GREBEAL INFORMATION:

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-240

CUTRENT PELING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/261,014

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR PILING DATE: 2001-01-11

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                                                                                                      Length 381;
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                                                                                              Query Match 92.3%; Score 1942; DB 15; Best Local Similarity 91.6%; Pred. No. 4.4e-153; Matches 351; Conservative 9; Mismatches 17;
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; ORGANISM: Homo sapiens
US-10-099-322-44
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ORGANISM: Homo sapiens
US-10-044-564-44
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LENGTH: 381
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## Sequence 42, Application US/10099322

## Publication No. US20030215449A1

## SPELICANT: Mezes et al.

## TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-240CIP

## CURRENT PILING DATE: 2002-911

## PRIOR APPLICATION NUMBER: 60/261,014

## PRIOR APPLICATION NUMBER: 60/261,014

## PRIOR APPLICATION NUMBER: 60/261,018

## PRIOR PILING DATE: 2001-01-11

## PRIOR PILING DATE: 2001-01-11

## PRIOR PILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                              APPLICANT: YOUNG, Paul
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Connective Tissue Growth Factor-4
FILE REFERENCE: PP467
CURRENT APPLICATION NUMBER: US/10/394,015
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US/09/325,019
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: SAPING DATE: 1999-06-05
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1938; DB 14;
Pred. No. 9.5e-153;
9; Mismatches 18;
     359 CPHANEAAFPFYRLFNDIHKFRD 381
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                                                                                                                           Sequence 5, Application US/10394015
Publication No. US20030180891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91,4%;
Matches 350; Conservative
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ORGANISM: Homo sapiens
US-10-394-015-5
                                                                                                                                                                              GENERAL INFORMATION
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CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLG 180
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                                                                             239 CSKTCGTGISTRVINDNPECRLVKETRICGVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                --LGLDASEVELTRNNELLAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKGIVQTTSWSQ
                                                                                                                                                                                                                                                   TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKWRPRCEDGEMFSKNVMMIQSCKCNYN
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TITLE OF INVENTION: Connective Tissue Growth Factor-2
FILE REFERENCE: PP126P102
CURRENT APPLICATION NUMBER: US/10/294,796
CURRENT FILING DATE: 2002-11-15
FRIOR PPLICATION NUMBER: US 09/348,815
FRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: ECT/US94/07736
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-12
NUMBER OF SEC 1D NOS: 6
SOFTWARE: Patentin version 3.1
SEQ 1D NO 2
LENGTH: 381
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Best Local Similarity 91.4%; Pred. No. 9.5e-153;
Matches 350; Conservative 9; Mismatches 18;
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Publication No. US20030078391A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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181 KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ 238
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| Sequence 2, Application US/10381644
| Publication No. US20040023910A1
| GENERAL INFORMATION:
| APPLICANT: American Home Products Corporation
| APPLICANT: Anany, Zhiming
| APPLICANT: Sampath, Deepak
| APPLICANT: Sampath, Deepak
| APPLICANT: Zhu, Yuan
| APPLICANT: Zhu, Yuan
| APPLICANT: Annex, Richard
| TITLE OF INVENTION: Use of Cyr61 in the treatment and
| TITLE OF INVENTION: Use of Cyr61 in the treatment and
| TITLE OF INVENTION: Use of Cyr61 in the treatment and
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| TITLE OF INVENTION: Use of Cyr61 in the treatment and
| TITLE OF INVENTION: Use 
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Pred. No. 9.5e-153;
9; Mismatches 18;
          PRIOR APPLICATION NUMBER: 60/261,029
PRIOR FLING DATE: 2001-01.1
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 306
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
LENGTH: 381
TYPE: PRT
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Best Local Similarity 91.4%;
Matches 350; Conservative
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US-10-044-564-42
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ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-240
CURRENT APPLICATION WINBER: US/10/044,564
CURRENT FILING DATE: 2002-09-09
FILOR PELICATION NUMBER: 60/261,014
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
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Best Local Similarity 91.4%; Pred. No. 9.5e-153;
Matches 350; Conservative 9; Mismatches 18;
PRIOR APPLICATION NUMBER: 60/318,410
PRIOR FILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PATENTIN VET: 2.1
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Publication No. US20040018196A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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US-10-044-564-42
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297 TYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKARFRCEDGEMPSKNVMAIQSCKCNYN 356
299 TYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKARFRCEDGETFSKNVMAIQSCKCNYN 358
                                                           179 -- LGLDASEVELTRINELIAIGKGSSLKRIPVFGTEPRVLFNPLHAHGOKCIVQTTSWSQ 236
                                                                                                                                                                                                           181 KELGFDASEVELTRNNELIAVGKGSSLKRLPVFGMEPRILYNPL--QGQKCIVQTTSWSQ 238
                                                                                                                                                                                                                                                      CSKSCGTGISTRVINDNPECKLVKRTRICEVRPCGQPVYSSLKKGKKCSKTKKSPBPVRF 296
                                                                                                                                                                                                                                                                        239 CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKKKKKSPEPVRF 298
                    1 MSSRIARALALVVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 22, 2004, 17:53:39; Search time 16.4566 Seconds (without alignments) 2215.320 Million cell updates/sec

US-09-495-448A-2 2103 1 MSSSTFRTLAVAVTLLHLTR......PNEASFRLYSLFNDIHKFRD 379 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:* 1: Dirl:* 2: Dirl:* 3: Dir2:* 4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	gene (YR61 protein	10 prot	prot	connective tissue	NOV protein - chic	gene_novH protein	hypothetical prote	mucin - rat	, submaxill	MEGF6 protein - ra	hypothetical prote	secreted leucine-r	5AC (clc	mucin MUC5B, trach	Balbiani ring 3 pr	mucin-like peptide	hypothetical prote	protein F40E10.4 [slit-1 protein hom	laminin B1k chain	notch4 - mouse	hypothetical prote		3	laminin alpha-2 ch	thrombospondin pre	adhesive plaque pr	ble vitellog	mucin 2 precursor,
SUMMARIES	ID	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	142	~	A40551	S20078	10	T26972	JC5598	T03099	T13954	T27283	T42626	A57534	A53767	S08167	A42112	T22025	D89711	T42218	A53612	T09059	T16840	A55035	T42215	S53868	0	617	T18308	393
	DB		101	N	N	N	N	N	N	0	N	N	N	N	N	N	~	N	N	0	~	7	~	~	ผ	М	Н	N	N	7
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insulin-like growt	MEGF5 protein - ra	hypothetical prote	probable laminin a	hypothetical prote	insulin-like growt	spore coat protein	notch protein homo	fibrillin 1 precur	jagged protein pre	notch protein homo	hypothetical prote	gene shuttle craft	hypothetical prote	galactose binding	Nel-homolog protei
148601	T13953	T23433	T37316	T27684	JN0508	S11676	A40043	A47221	A56136	S18188	T18649	T13938	T44598	T09229	T10756
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135.5		135	135	134	133.5	133.5	133.5	133.5	133	133	132.5	132.5	132.5	132	131.5
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ALIGNMENTS

RESULT 1

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A40578
A41078
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A40578: Mouse mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #text_change 01-Dec-2000
C;Accession: A40578; A53228
R;Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.
DNA, Cell Biol. 10, 293-3300, 1991
A;Tille: Identification of a gene family regulated by transforming growth factor-beta.
A;Reference number: A40578; MUID:91229699; PMID:2029337
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                                                                            CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKNRPRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVKKYRPKYGGSCVDGRCCTPQQTRTVKIRFRCDDGBIFTKSVMMIQSCRCNYNCPHANE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                     CEF-10 protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Bate: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jul-2000
C;Accession: A41428
R;Simmons, D.L; Levy, D.B.; Yannoni, Y.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
A;Title: Identification of a phorbol ester-repressible v-src-inducible gene.
A;Reference number: A41428; MUID:89145206; PMID:2537491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CGTGISTRVTNDNPBCRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALAAALLCLARLALGSPCPAVCQCPAAAPQCAPGVGLVPDGCGCCKVCAKQLNEDCSRTQ
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 CGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG
                                                          CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKARFRCEDGEMFSKAVAMIQSCKCNYNCPHP
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Best Local Similarity 80.1%; Pred. No. 3.1e
Matches 302; Conservative 22; Mismatches
                                                                                                                    NEASFRLYSLFNDIHKFRD 379
                                                                                                                                      A-YPFYRLVNDIHKFRD 375
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                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-375 <SIM>
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A Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-348 «BRU>
A, Cross-references: GB M80263; NID:g201945; PIDN:AAA73135.1; PID:g201946
A, Cross-references: GB M80263; NID:g201945; PIDN:AAA73135.1; PID:g201946
B, Ryseck, R. P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Cell Growth Differ: 2, 225-233, 1991
A, Title: Structure, mapping, and expression of fisp-12, a growth factor-inducally A, Reference number: A53228; MUID:91363290; PMID:188698
A, Resession: A53228
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-160, K', 162-348 <RYS>
A, Coss-references: GB:M70641; NID:g193313; PIDN:AAA37627.1; PID:g193314
A, Genetics:
A, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 XHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCBEWVCDFDSIXDSLDDQDD
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A; Accession: S44205
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-349 < COEM>
A; Cross-references: EMBL:X78947; NID:g474933; FID:g474934
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45.5%; Score 957.5; DB 2;
Best Local Similarity 46.8%; Pred. No. 1.5e-60;
Matches 178; Conservative 60; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPGDNDIFESLYYRKMYGDM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPHPNEASFRLY -- SLFNDI 374
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Cispecies: Home sapiens (man)
Cispecies: Jacoba desequence_revision 17-May-1996 #text_change 05-Nov-1999
Cispecies: Jacoba desequence_revision 17-May-1996 #text_change 05-Nov-1999
Rivartinerie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunders, G.; Strong, L.; Perbal Aritics: Structural analysis of the human nov proto-oncogene and expression in Wilms tu A; Reference number: Ja8069; MUID:94386229; PMID:7520150
A; Accession: I38069
A; Accession: I38069
A; Accession: Lype: DNA
A; Residues: Ja57 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
211 ACSKSCGMGFSTRVTNRNQQCEMVKQTRLCMMRPCENBEPSD-KKGKKC1QTKKSMKAVR 269
                                                                                       CKVCAKQLNEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CLVCARQRGESCSDLEPCDESSGLYCDRSADPSNQTGLCTA-VEGDNCVFDGVIYRSGEK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 FQPNCKHQCTGIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 SWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKOVMMIQSC 351
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C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T26972
R;Harris, B.
                                                                  FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMM1QSCKCNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VQSTSFCLRKQCLCLTFLLLHLLGQVAATQRCPPQCPGRCPATPPTCAPGVRAVLDGCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSSSTF----RILAVAVTLLHLTRLALST--CPAAC--HCPLEAPKCAPGVGLVRDGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X78351; NID:g587422; PIDN:CAA55146.1; PID:g825696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 DDQDDLLGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 GG----LTLAAYRPEATLGVEV----SDSSV------------NCIEOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: novH
A;Introns: 28/3; 104/1; 188/1; 259/3
A;Introns: 28/3; 104/1; 188/1; 259/3
C;Superfamily: thrombospondin type 1 repeat homology
F;203-250/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.9%; Score 839.5; DB 2; Best Local Similarity 43.8%; Pred. No. 3.3e-52; Matches 163; Conservative 52; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 KCNYNCPHPNEA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 TCHTNCPKNNEA 343
                                                                                                                                                  356 NCPHPNEASFR 366
                                                                                                                                                                                         NCPOSNNAFFO 340
                                                                                                                                                                                                                                                                                                     gene novH protein - human
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Cybecies: Gallus gallus (chicken)
Cybecies: Gallus gallus (chicken)
Cybecies: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
Cybecssion: S20078
Cybecies: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
Cybecssion: S20078
Cybecssion of a new cellular gene (nov) in myellaritie: Proviral rearrangements and overexpression of a new cellular gene (nov) in myellaritie: Proviral rearrangements and overexpression of a new cellular gene (nov) in myellaritie: Proviral rearrangements and overexpression of Aprecession: S20078
AyReference number: S20078
AyStatus: preliminary
AyMolecule type: mRNA
AyResidues: 1-351 < JOL>
AyConetics:
CyGenetics:
CyGenetics:
AyGene: Nov
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                                                                                                                                                                                                                                                                              FQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSL 172
                                                                                                                                                                                                                                                                                                                                                                   231
                                                                                                                                                                                                                                                                                                                                                                                                          -DQ-----RANCLVQT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 TSWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLOTRTVKMRFRCEDGEMPSKNVMMIQSC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESCSPLLPCDESGGLYCDRGPEDGGGAGICMV-LEGDNCVFDGMIYRNGETFQPSCKYQC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCD-EDSI-----KDSLDDQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDLLGLDASEVELTRNNELLAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNCKHOC 121
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                                                                                                                                                99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LPVILLILLILRPCEVSGREAACPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCARQRG 68
                                                                                                                                  DDQDDLLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQT
                                                                                                    1 MSSSTFRTLAVAVTLLHLTRLALSTCPAA-----CHCPLE-APXCAPGVGLVRDGCGC
                                                             Gaps
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                                                                48;
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                      Length 349;
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44.5%; Pred. No. 9.9e-54;
ive 44; Mismatches 110; Indels
                                                             97; Indels
                      5
                  Query Match
45.2%; Score 950; DB 2;
Best Local Similarity 45.7%; Pred. No. 5e-60;
Matches 176; Conservative 64; Mismatches 5
                                                             64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 ACHYNCPGDNDIFESLYYRKWYGDM 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 KCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.5
Matches 165; Conservative
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us-09-495-448a-2.rpr

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A; Molecule type: mRNA

A; Residues: 1-13288 cEC.>

A; Residues: 1-13288 cEC.>

A; Cross-references: EMB1: AF005273; NID: 92581863; PIDN: AAC62527.1; PID: 92581864

B; Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.

C. Balol. Chem. 266, 9678-9686, 1991

A; Title: Porcine submaxillary mucin contains a cystine-rich, carboxyl-terminal domain i

A; Reference number: A40009; MUID: 91236743; PMID: 2033060
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A;Cross-references: GBNM1174; GB:G03512; NID:g164321; PIDN:AAA30990.1; PID:g552360
A;Experimental source: submaxillary gland
R;Eckhardt, A.E.; Timpte, C.S.; Abernethy, J.L.; Toumadje, A.; Johnson Jr., W.C.; Hill,
                                                                                                                                                                                                                                                                                                                                                                        NCKHQCTCIDGAVGC-IPLCPQELSLPNLGCPNPRLVKVS-----GQCCSEWVCDEDSIK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERCLCEVSSNAFSDVFVVNCETELCNTQCPKGFEYQTTPGHCCGQCVPKTCPFKNSNNST 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -VYSSLK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||: :: :: |
PQQXCTVHQRQ-QIIR--QQNC88EGPVSLSYCQGNCGDSTSMYSLEANTVEHTCECCQE 958
                                                                                                                                                                                                                                                                                                                                                                                                                        NCQ-DCICKEGTLTCQEKLCPQPT-----CPEPGFVPVSIALEAGQCCSQFSC---VC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSLDDQDDLLGLDASEVELTRNNELIAIGKG-SSLKRLPVFGTEPRVLFNP----LHAHG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --NDNPEC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           842 SLYKPGEFWPEPGNPCVTHKCEKFODVLTVVTVXIECPKINCPODWAQLREDGCCYDCLV 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RCCTP 323
                                                                                                                                                                                                                                                                                               RNDDISLSLAIQKAGPKSEGCFCPDDMTLFSSNDSICVPSCQWCLGPHGEPVEPGHTISI
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                                                                                                                                                                                                             CHM-LDLEVVCSGLELYASLCAAQGVCIPWRSHTNNTCPFTCPENQVYQPCGPSNPHYCY
                                                                                                                                                             30 CHCPLEAPKCAPGVGLVRDGCGCCKVC---AKQLNEDCSKT-----QPCDHTKGLECN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGASSTALKGICRA--QSEGRPCEYNSRIYQ------NGESFQP----
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
A, Residues: 12139-12167, T', 12169-13288 <BC3>
A, Residues: 12139-12167, T', 12169-13288 <BC3>
A, Crose: references: GB M61883; NID: g454837; PIDN: AAA30998.1; PID: g164374
R; Timpte, C.S.; Bckhardt, A.B.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988
A, Title: Porcine submaxillary gland apomucin contains tandemly repeated, A, Reference number: A28528; MUID: 88087170; PMID: 2826455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mucin, submaxillary - pig

Mixlernate names: apomucin

Cispecies: sus scrofd admestica (domestic pig)

Cispecies: Sus scrofd admestica (domestic pig)

Cibate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Jun-1

Circession: T03099; A40009; A28528; B29789

Circession: T03099; A40009; A28528; B29789

Airtle: The complete cDNA sequence and structural polymorphism of the paracesence number: Z14839; MUID:98070526; PMID:9407109

Aixecession: T03099

Aixcession: T03099

Aixecession: T03099
  F;762-830/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                        Indels 146;
                                                     Length 1034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 KGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYC-GSCVDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOTRIVKMRFRCEDGEMFSKNVMMIQSCKC-NYNCPHPNEAS 364
                                                     ; Score 166; DB 2; L; Pred. No. 0.00035; 47; Mismatches 170;
                                                     7.9%;
ilarity 21.4%;
Conservative 4'
                                                     Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A28528
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A;Map position: 1
A;Introns: 50/2; 84/2; 150/1; 238/3; 342/3; 797/1; 851/1; 947/2; 1017/1; 1083/1
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Residues: 1-1034 < LINA>
A/Cross-references: GB:U83139; NID:g2315984; PIDN:AAC53312.1; PID:g2315985
A/Cross-references: Cmplete
C/Comment: This protein is a high molecular weight glycoprotein which is a major component: This protein is a high molecular weight glycoprotein which is a major component tract and reproductive tract.
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                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1111 <WIL>
A;Residues: 1-1111 <WIL>
A;Cross-references: EMBL:AL032657; PIDN:CAA21739.1; GSPDB:GN00019; CESP:Y47H9C.4
A;Experimental source: clone Y47H9C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                           20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NPRLVKVSGQCCEEWVCDEDSIXDSLDDQDDLLGLDASEVELTRNNE 193
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C;Date: 23.Sep-1997 #sequence_revision 23.Sep-1997 #text_change 05-Nov-1999
C;Date: 23.Sep-1997 #sequence_revision 23.Sep-1997 #text_change 05-Nov-1999
C;Accession, T.;Tisdale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.
Biochem. Biophys. Res. Commun. 236, 789-797, 1997
A;Title: Cloning of rat MucSAC mucin gene: Comparison of its structure and the Ricerence number: UC5598; MUID:97396181; PMID:9245735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTC-----IDGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPAACHCPLE-APKCAPGVGLVR----DGCGCCKVCAK-QLNEDCSKTQPCDHTKGLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSKTCTCVRENTLMCAPNTGFCRCKPGFYGDNCELACSKDSYGPNCEKQAMCDWNHASEC
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                                                                                                                                                                                                                                                                                                                                                                  8.1%; Score 171; DB 2; Length 1111;
20.1%; Pred. No. 0.00017;
ative 32; Mismatches 156; Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 TNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 SYGPGCKLHCKCVNGKCDKETGEC----TC-----QPGFFGSDCS-
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C;Superfamily: von Willebrand factor type C repeat homology
F;45-149/Domain: cysteine-rich <CYS>
submitted to the EMBL Data Library, October 1998
A;Reference number: 220293
A;Accession: T26972
                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 20.19
86; Conservative
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Best Local S
Matches 86
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us-09-495-448a-2.rpr

93 GCCKVCAKQL	RESULT 11 T27233 hypothetical protein Y64G10A.f Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 12. Cot. 1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999 R; Ainscough, R. Spicession: T27233 R; Ainscough, R. Spicession: T27233 A; Accession: T27233 A; Molecule type: DNA A; Reference number: 23.336 A; Molecule type: DNA A; Residuces: 1.160 c/MLL. A; Cross-references: EmBL:Ail10498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f A; Gene: CESP:Y64G10A.f A; Ge	1207NGDCECIDGWTGPSLCPFGGFGRNCAGRCN-CKNGA 226 KCIVQTTSWGQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSS
J. Biol. Chem. 262, 11339-11344, 1987 A,Title: Structural properties of porcine submaxillary gland apomucin. A,Reference number: A92606; MUID:87280230; PMID:3611111 A,Accession: B29789 A,Molecule type: protein A,Residues: 1572-1607 < EC2> C,Superfamily: pig submaxillary mucin C,Keywords: tandem repeat Query Match Query Ma	QY 221 HAHGGKC	Query Match Best Local Similarity 20.4%; Pred. No. 0.0024; Matches 94; Conservative 40; Mismatches 142; Indels 185; Gaps 24; Qy 26 CPPAACHCPLEAPKCAPCV-GLVRDGC

DD 1239 GCOCDEWRGEKCONE TO THE CONTRIBUTION OF	### Pasturr 13 ### ### ### ### ### ### ### ### ### ##
Oy 348 IQSCKC 353 : Db 1015 VVKCGC 1020	A53767 mucin MUCSB, tracheobronchial - human C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Apr-2000 C;Accession: A53767

579

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628 GQKWNDRVC-SC---GCPVP------RPDCTNGQIYN-----INTCACGCGIDKPSCP 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 LKGICRAQSEGRPCEYNSRIYQNGESFQP-NCKHQCTCIDGAVGC-----IPLCPQE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 CKCVCPADKOMSPGGCGS----GKSFNKLTC--OCECDOSASKCGLKRWNADTCKCECO 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 LSLPNLGCPNPRLV--KVSGQCCEEWVCDEDSIKDSLDDQDDLLGLDASEVE----LTR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 VKKYRPKYCGSCVDGRCCTPLQTRTVKARRRCEDGEMFSKNVMMIQSCKCNYNCPHPNEA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 PGMPPEGCGKQTWISDKCKCECSPTITCOAPQILD-----LNTCECKCPVNMLAQ 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 NNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQC----SKSCGTGI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 STRVTNDNPECRLVKETRICEVRP-CGQP-VYSSLKKGKKCSKTKKSPEPVRFTYAGCSS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 CHCPLEAPKCAPGVGLVRDGCG -- C-CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 -NKKFFDKPSCECK-----CKNNPTCTSPQVWDADDCECKCPKDKQKPQ------GGGCDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               531 KEKCKSPROWIDSKCLCECSTIPATCEGKOIWCGEAC------OCICPGGDKNCG---
                                                                                                                                                                       A;Status: not compared with conceptual translation
A;Nolecule type: DNA
A;Residues: 1-1700 cPAU>
A;Residues: 1-1700 cPAU>
A;Cross-references: GB:X52263; NID:g7057; PIDN:CAA36506.1; PID:g7058
C;Genetics:
A;Gene: BR3
A;Gene: BR3
A;Map position: 4
C;Superfamily: unassigned Balbiani ring proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 151.5; DB Best Local Similarity 22.7%; Pred. No. 0.0058; Matches 83; Conservative 41; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: April 22, 2004, 17:59:21
Job time : 19.4566 secs
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RESULT 15
508167
Balbiani ring 3 protein - midge (Chironomus tentans)
C;Species: Chironomus tentans
C;Species: Chironomus tentans
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
B;Paculsson, G; Lendahl, U; Galli, J; Ericsson, C; Wieslander, L.
J; Mol. Biol. 211, 331-349, 1990
J; Mol. Biol. 211, 331-349, 1990
A;Fitle: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive struct A;Reference number: S08167, MUID:90172404; PMID:1689777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | : | : | | : | | | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 HGQKCIVQTTSWSQC-----SKSCGT----SKSCGT----GISTRVTND 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.2%; Score 152; DB 2; Length 10; Best Local Similarity 19.1%; Pred. No. 0.0035; Matches 107; Conservative 57; Mismatches 152; Indels
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OM protein - protein search, using sw model

April 22, 2004, 17:52:34; Search time 10.4724 Seconds (without alignments) 1884.444 Million cell updates/sec Run on:

US-09-495-448A-2 2103 1 MSSSTFRILAVAVTLHLTR......PNEASFRLYSLFNDIHKFRD 379 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	CYR6 MOUSE	CYR6 RAT	CYR6 HUMAN	CE10 CHICK	CTGF RAT	CTGF WOUSE	CTGF HUMAN	CTGF_BOVIN	CTGF_PIG	NOV CHICK			NOV_RAT	NOV MOUSE	NOV_XENLA	WSP1 HUMAN	WSP1_MOUSE	WSP1_RAT	WSP3_HUMAN	WSP2_MOUSE	WSP2_HUMAN	WSP2_RAT	SLT2_HUMAN	NRL1_MOUSE	NRL1_CHICK	LMA2_HUMAN	MUSA HUMAN	BAR3_CHITE	NRL1_HUMAN	MUCL_RAT			LRP2_HUMAN
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ð	Query Match	0	98.9	N	œ	45.6	45.5	45.2	44.6	43.7	40.9		39.9			39.5		36.1		29.6							•	•	•	•	•	6.9	•	•
	Score	2103	2079	1938	1646.5	960	957.5	950	937	919	861	856	839.5	829.5	827	824.5	773	758.5	757	622	526.5	524	492	166	158	154	154	152.5	151.5	148	146	145.5	144.5	144
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Q28833 sus scrofa Q13751 homo sapien	Q9y6nb nomo sapien 088799 mus musculu P57999 oryctolagus	Q60675 mus musculu P35440 gallus gall Q25464 mytilus gal	P31695 mus musculu Q02817 homo sapien	Q9r118 mus musculu P47877 mus musculu
VWF PIG	LMG3 HUMAN ZAN MOUSE ZAN RABIT	LMAZ MOUSE TSP2 CHICK FP2 MYTGA	NTC4 MOUSE MUC2 HUMAN	HRAI MOUSE IBP2_MOUSE
				
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143	141 141 140.5	140 139.5 139	138	136 135.5
9. S.	3.76 3.76	6 4 4 6 0 1	443	4 4 5

ALIGNMENTS

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immediate early growth requirery game CYR61.";

U. Biol. Chem. 275:28929-28936(2000).

U. Biol. Chem. 275:28929-28936(2000).

I. FUNCTION: Promotes cell proliferation, chemotaxis, angiogenesis and cell adhesion. Appears to play a role in wound healing by upregulating, in skin fibroblasts, the expression of a number of genes involved in angiogenesis, inflammation and matrix remodeling including VBGA-A, VBGA-C, MMP1, MMP3, TIMP1, uPA, PAI-1 and incepting alpha-3 and alpha-5 (By similarity). Cyr61-mediated gene regulation is dependent on heparin-binding (By similarity). Downregulation is dependent on heparin-binding (By similarity). Downregulates the expression of alpha-1 and alpha-5 subunits of collagen type-1 (By similarity). Promotes cell adhesion and adhesive signaling through integrin alpha-1/beta-3 and cell proliferation through integrin alpha-1/beta-3 and cell proliferation through integrin alpha-1/beta-3 and cell proliferation through integrin alpha-1/beta-3 (By similarity).

SUBUNIT: Interaction with integrins is heparin- and cell-type-dependent and promotes cell adhesion (By similarity).

SUBJUARITY: Belongs to the CCN femily.

SIMILARITY: Contains I TGPB domain.

SIMILARITY: Contains I TSP type-1 domain.

SIMILARITY: Contains I TSP type-1 domain.
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LDASEVELTRANGELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKS 240
                                                                                                                 241 CGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG 300
                                                                                                                                                                          301 CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
                                                                                                                                                                                                            CSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHP 360
                                                                        CGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAG 300
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MEDLINE-20435857; PubMed=10852911;
Albrecht C., von Der Kammer H., Mayhaus M., Klaudiny J., Schweizer M.,
Nitsch R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Muscarinic acetylcholine receptors induce the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CTT-2003 (Rel. 42, Last annotation update)
CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61)
(Insulin-like growth factor-binding protein 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                           379 AA.
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InterPro; IPR006207; Cys knot C.
InterPro; IPR000867; Tnsl gro_fac_pr.
InterPro; IPR000884; TsPl.
                                                                                                                                                                                                                                                                       361 NEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                         361 NEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                               181
                                                                             241
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Q9ES72;
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-!- DEVELOPMENTAL STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1) IN NORMAL CELLS, AND AT A CONSTANT LEVEL IN RAPIDLY GROWING CELLS.
-!- INDUCATION: By growth factors family.
-!- SIMILARITY: Belongs to the CCN family.
-!- SIMILARITY: Contains 1 URFP domain.
-!- SIMILARITY: Contains 1 TYP type-1 domain.
-!- SIMILARITY: Contains 1 TYP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSP TYPE-1.
HEPARIN-BINDING.
CTCK.
BY SIMILARITY.
W, FAGES014B56A8EE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:88613; Cyr61.

GO; GO:0001569; P:patterning of blood vessels; IMP.
InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot_C.
InterPro; IPR00867; Insl_gro_fac_pr.
InterPro; IPR000867; INSl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2103; DB 1; ilarity 100.0%; Pred. No. 2.3e-156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYR61 PROTEIN.
VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART, SM00214; VWC; 1.
PROSITE, P801185; CTCK 1; 1.
PROSITE; P801225; CTCK 2; 1.
PROSITE; P800222; IGF BINDING; 1.
PROSITE; P800022; ISFI, 1.
PROSITE; P801208; VWFC 1; 1.
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EMBL; X56790; CAA40109.1; -.
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_knot; 1.
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Pfam; PF00007; Cys Knot;
Pfam; PF00219; IGFBP; 1.
Pfam; PF00099; tsp_1; 1.
Pfam; PF00093; vwc; 1.
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SMART; SM00121; IB; 1.
SMART; SM00209; TSP1;
SMART; SM00214; VWC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A35669; A35669.
MGD; MGI:88613; Cyr6
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                                                                        SEQUENCE FROM N.A.
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                   nomus vagitans (numan).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"Organization and expression of the CYR61 gene in normal human
                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
Kolesnikova T.V., Lau L.F.;
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cells from the nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11584015;
 OR IGFBP10 OR CCN1 OR GIG1.
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Chen C.-C., Mo F.-E., Lau L.F.;
                                                                                                                                                                                                                                                                                                Mol. Pathol. 50:310-316(1997)
                                                                                                                                                                                             to chromosome lp.";
Oncogene 14:1753-1757(1997).
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               sapiens (Human)
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                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                          Growth factor binding, Heparin-binding,
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TSP TYPE-1.
HEPARIN-BINDING (BY SIMILARITY).
CTCK.
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000622: 014934; 043775; 098ZL7;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
CYR61 protein precursor (Cysteine-rich, updiogenic inducer, 61)
(Insulin-like growth factor-binding protein 10) (GIG1 protein).
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Pred. No. 1.7e-154;
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         PEGMI, PF00007; Cyg Knot; 1.
PEAM; PF00129; IGFBP; 1.
PEAM; PF00129; IGFBP; 1.
PEAM; PF00099; vwc; 1.
SWART; SW00041; CT; 1.
SWART; SW00121; IEP; 1.
SWART; SW00121; IEP; 1.
SWART; SW00214; Vwc; 1.
PROSITE; PS01185; CTCK, 1.
PROSITE; PS01225; CTCK, 2; 1.
PROSITE; PS01225; TSP1; 1.
PROSITE; PS01029; VWFC_2; 1.
PROSITE; PS01094; VWFC_2; 1.
PROSITE; PS01194; VWFC_2; 1.
PROSITE; PS01194; VWFC_2; 1.
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 InterPro; IPR001007; VWF
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379 AA;
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Matches 350; Conservative
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SMART; SM00121; IB; 1.
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REDINE-21293087; PubMed=11287419;

REDINE-21293087; PubMed=11287419;

RET GreasAid-waicz T.M., Kirschling D.J., Chen N., Lau L.F.;

RET GreasAid-waicz T.M., Kirschling D.J., Chen N., Lau L.F.;

RET GreasAid-waicz T.M., Kirschling D.J., Chen N., Lau L.F.;

Alpha vbeta 5 and enhances mitogenesis through integrin alpha vbeta

RET J. independent of its carboxyl-terminal domain.";

RET J. independent on heparin-binding. Down-regulated gene regulation is dependent on heparin-binding. Down-regulates the expression of a long-alpha-1 and alpha-3 and alpha-5. Cyr61-mediated gene regulation is dependent on heparin-binding. Down-regulates the expression of a long-alpha-1 and alpha-2 subunits of collagen type-1. Promotes cell migration through integrin alpha-V/beta-3.

CC -1 SUBULIATI Interaction with integrin alpha-V/beta-3.

CC -1 SUBCELLUAR LOCATION: Secreted.

CC -1 SUBCELLUAR LOCATION: Secreted.

CC -1 SUBCELLUAR LOCATION: Secreted.

CC -1 SUBLIARITY: Contains 1 UWFC domain.

CC -1 SIMILARITY: Contains 1 UWFC domain.

CC -1 SIMILARITY: Contains 1 UWFC domain.
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MEDLINE=20387398; PubMed=10821835;
Chen N., Chen C.-C., Lau L.F.;
"Adhesion of human skin fibroblasts to Cyr61 is mediated through integrin alpha6betal and cell surface heparan sulfate proteoglycans.";
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                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH INTEGRIN ALPHA-IIB/BETA-3.
MEDLINE=99377072; PubMed=10446209;
Jedsadayanmata A., Chen C.-C., Kreeva M.L., Lau L.F., Lam S.C.;
"Activation-dependent adhesion of human platelets to Cyr61 and
Fispl2/mouse connective tissue growth factor is mediated through
integrin alpha(IIb)Deta(3).";
J. Biol. Chem. 274:24321-24327(1999).
                                                                                                                                                                                                      Kireeva W.L., Lam S.C., Lau L.F., "Adhesion of human umbilical vein endothelial cells to the immediate-early gene product Cyr61 is mediated through integrin
                                                                                                                                            INTERACTION WITH INTEGRIN ALPHA-V/BETA-3
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                                                                                                                                                                                                                                                                                  alphavbeta3.";
J. Biol. Chem. 273:3090-3096(1998)
[11]
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EMBL; EMBL; EMBL;

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDBDSIKDSLDDQDDL-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEDCSKTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFOPNCKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 --LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 CSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSSSTFRTLAVAVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
                                                                                                                                                                                                                                                                                                        PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01029; TSPI; 1.
PROSITE; PS10209; WRFC_1; 1.
PROSITE; PS10184; WRFC_2; 1.
Chemotaxis; Cell adhesTon; Growth factor binding; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSP_TYPB-1.
HEPARIN-BINDING (BY SIMILARITY)
CTCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.2%; Score 1938; DB 1; Length 381; 91.4%; Pred. No. 1.5e-143; ive 9; Mismatches 18; Indels
E -> Q (IN REF. 3).
L -> R (IN REF. 5).
L -> R (IN REF. 5).
F -> L (IN REF. 7).
W, FCOBD39C078CAOBI CRC64;
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CYR61 PROTEIN.
IGPBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                        375 AA
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SIMILARITY.
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TSP TYPE-1.
CTCK.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J04496; AAA46661.1;
PIR; A41428; A41428.
InterPro; IPR006208; Cys knot.
InterPro; IPR006208; Cys knot.
InterPro; IPR006867; Insl_gro_fac_pr.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000867; VWF_C.
Pfam; PF00007; Cys knot; 1.
Pfam; PF00097; VWF_C.
Pfam; PF00090; Vxc; 1.
SWART; SW000219; IGPBP; 1.
SWART; SW000219; ISP1: 1.
SWART; SW00219; ISP1: 1.
SWART; SW00219; ISP1: 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01208; VWFC_2; 1.
PROSITE; PS01208; VWFC_2; 1.
PROSITE; PS01208; VWFC_2; 1.
PROSITE; PS01208; VWFC_2; 1.
359 CPHANEAAFPFYRLFNDIHKFRD 381
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89145206; PubMed=2537491;
                                                                                                                               CEF-10 protein precursor
                                                                        STANDARD;
                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                        CHICK
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DISULFID
DISULFID
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Trezuka K., Tamatani T.,

"Rattus norvegicus connective tissue growth factor ";

"Rattus norvegicus connective tissue growth factor ";

"Uminted (PEB-199) to the EMBL/GenBank/DDBJ databases.

"Uminted (PEB-199) to the EMBL/GenBank and databases.

"Uminted (PEB-199) to the CMB family.

"Uminted (PEB-199) to the CMB fa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 SVKKYRPKYCGSCVDGRCCTPQQTRTVKIRFRCDDGETFTKSVMMIQSCRCNYNCPHANE 359
                                                                                                                                                                                                                                                                                                                                                                                                 129 GCIPLCPQELSLPNLGCPNPRLVXVSGQCCEEWVCDEDSIKDSLDDODDL----LGLDAS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
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MEDLINE=2014-5935; PubMed=10679821;
Xu J., Smack S.L., Safadi F.P., Rosenzweig A.B., Odgren P.R.,
Marks S.C. Jr., Owen T.A., Popoff S.N.;
"Cloning the full-length cDNA for rat connective tissue growth factor:
"Indications for skeletal development.";
jmplications for skeletal development.";
Cell. Biochem. 77:103-115(2000).
                                                                                                                                                                                                                                                                                                                     69 PCDHTKGLECNFGASPAATWGICRAQSEGRPCEYNSKIYQNGESFQPNCKHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 EGELTRNNELIAIVKG-GLKMLPVFGSEPQSRAFENP-----KCIVQTTSWSQCSKTCG
                                                                                                                                                                     10 AVAVTLIHLTRLAL-STCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQ
                                                                                                                                                                                                                            9 ALAAALICLARLALGSPCPAVCQCPAAAPQCAPGVGLVPDGCGCCKVCAKQLNEDCSRTQ
                                                                                                                                                                                                                                                                                   PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 EVELTRINBELIAIGKGSSLKRLPVFGTEP--RVLFNPLHAHGQKCIVQTTSWSQCSKSCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                           17; Gaps
                                                       DB 1; Length 375;
                                                                                                              Indels
375 AA; 40651 MW; 95F28553BE35D5AE CRC64;
                                                                                                                 36;
                                                    78.3%; Score 1646.5; DB 1, 80.1%; Pred. No. 6.7e-121; ive 22; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGF RAT STANDARD; PRT; 347 AA. Q9R1E9; Q9WVS1; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Connective Lissue growth factor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 ASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 A-YPFYRLVNDIHKFRD 375
                                                                                                              Conservative
                                                    Query Match
Best Local Similarity
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                                                                                                                 Matches 302;
                                                                                                                                                                                                                                                                                      69
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   SECUENCE
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298 YAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNC 357
                                                                                                                                  PHPNEASFRLY -- SLFNDI 374
                                                                                                                                                                                                    PGDNDIFESLYYRKMYGDM 346
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                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                      358
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                            R EMBL; AR120275; AAD39132.1; -...
R EMBL; AR023068; BAA83125.1; -...
R InterPro; IPR0066208; Cys_knot. C.
R InterPro; IPR0066208; Cys_knot. C.
R InterPro; IPR001007; Cys_knot. C.
R InterPro; IPR001007; VWF_C.
R InterPro; IPR001007; VWF_C.
R Pfam; PF001097; VWF_C.
R Pfam; PF00099; tsp_1:
R Pfam; PF00099; tsp_1:
R Pfam; PF00099; Tsp_1:
R SMART; SM00121; IB; 1:
R SMART; SM00121; IB; 1:
R SMART; SM00121; IB; 1:
R SMART; SM00204; TSP_1:
R RAPAT; SM00204; TSP_1:
R RAPAT; SM00204; TSP_1:
R RAPAT; SM00204; TSP_1:
R RAPAT; SM00202; TSP_1:
R PROSITE; PS01020; TSP_1:
R PROSITE; PS01089; VWFC_2:
R PROSITE; PS01084; VWFC_2
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       SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSSSTRRILAVAVTLIHLTRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCAK
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CONNECTIVE TISSUE GROWTH FACTOR
IGPBF.
VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.6%; Score 960; DB 1; Length 347; 46.4%; Pred. No. 1.4e-67; ive 61; Mismatches 104; Indels
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HEPARIN-BINDING (BY S. CTCK.
BY SIMILARITY.
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347 AA;
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MEDLINE=22388257, PubMed=12477932;

Atlauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atlauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atlauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Antschork D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Patherly J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakeeley R.W., Touchman J.W., Green B.D., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse cDNA sequences.",

"The Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
268 LSGCTSVKTYRAKFCGVCTDGRCCTPHRITTLPVEFKCPDGEIMKGNMMFIKTCACHYNC 327
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Kireeva M.L., Latinkic B.V., Kolesnikova T.V., Chen C.C., Yang G.P., Abler A.S., Lau L.F.;
"Cyrel and Fispl2 are both ECM-associated signaling molecules: activities, metabolism, and localization during development.";
Exp. Cell Res. 233:63-77(1997).
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Babic A.M., Chen C.C., Lau L.F.;
"Fisp12/mouse connective tissue growth factor mediates endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=91229699; PubMed=2029337;
Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;
"Identification of a gene family regulated by transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91362290; PubMed=1888698; Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.; Structure, mapping, and expression of fisp-12, a growth factorinducible gene encoding a secreted cysteine-rich protein."; Cell Growth Differ. 2:225-233 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                    P39268, 022200, 124, Created)
28-FEB-2003 [Rel. 41, Last sequence update)
10-0CT-2003 [Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rissup growth factor precused; [RISP-12 protein]
10-0CT-2004 (Rissup growth factor protein 24)
10-0CT-2004 (Rissup Growth factor protein 24)
10-0CT-2004 (Rissup Growth factor protein 24)
10-0CT-2005 (Rissup Growth factor protein 24)
10-0CT-2003 (Rel. 41, Last annotation update)
10-0CT-2003 (Rel. 41, La
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us-09-495-448a-2.rsp

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TISSUE=Umbilical vein endothelial cells;

MEDINE=93187114; PubMed=1293144;

Igarashi A., Bradham D.M., Okochi H., Grotendorst G.R.;

"Connective Lissue growth factor.";

J. Dermatol. 19:642-643 (1992).
                                                                                                                                                                                                    Score 957.5; DB 1;
Pred. No. 2.2e-67;
                                                                                                                                                                                                                                                 60; Mismatches 103;
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                                                                                                                                                       37794 MW;
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Best Local Similarity 46.89
Matches 178; Conservative
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348 AA;
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cell adhesion and migration through integrin alphavbeta3, promotes endothelial cell survival, and induces angiogenesis in vivo.";
Mol. Cell. Balol. 19:2588-2966(1999).
-! FUNCTION: Major connective tissue mitoattractant secreted by vascular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediates heparinand divident cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endothelial and epithelial cells (By similarity). Enhances fibroblast growth factor-induced DNA synthesis (By similarity).
-! SUBUNIT: Monomer (By similarity).
-! SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                       soluble form.

-! TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN
-! CLOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).
-!- INDUCTION: By growth factors.
-!- SIMILARITY: Belongs to the CCN family.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA synthesis; Extracellular matrix; Heparin-binding;
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EMBL; M70641; AAA37627.1; ---

EMBL; M70641; AAA31628.1; ---

EMBL; M70642; AAA43162.1; ---

EMBL; M0066783; AAA416783.1; ---

EMBL; BC066783; AAA7318.1; ---

EMBL; M0059537; Ctgf.

M005; M01:95537; Ctgf.

M005; M01:95537; Ctgf.

M005; M01:95537; Ctgf.

M005; M01:95537; Ctgf.

M005; M0010578; Fintegrin binding; IDA.

M005; M0010578; Fintegrin binding; IDA.

M005; M0010578; Fintegrin binding; IDA.

M005; M0010529; Fintegrin-mediated signaling pathway; IDA.

M005; M0010503; Ficell-matriand; IMP.

M005; M0010503; Ficell-matriand; IMP.

EMBL; M0010503; M001050
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HEPARIN-BINDING (BY SIMILARITY)
CTCK.
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TISSUE-Umbilical vein endothelial cells;

MEDLINE=91373462; PubMed=1654338;

Bradham D.M., Igarashla., Potter R.L., Grotendorst G.R.;

"Connective tissue growth factor: a cysteine-rich mitogen secreted by human vascular endothelial cells is related to the SRC-induced immediate early gene product CEF-10.";

J. Cell Biol. 114:1285-1294(1991).
                                                                                                                                                                                                                                                                    1 MSSSTFRTLAVAVTLIHL-TRLAL-STCPAACHCPLE-APKCAPGVGLVRDGCGCCKVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 KQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNC
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                                                                                                                                  Gaps
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                          39;
Length 348;
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FUNCTION

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53 CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES 112
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                                                                                                                                                                                                    SWART; SW00041; CT; 1.
SWART; SW00121; IB; 1.
SWART; SW01214; VWC; 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01225; CTCK 1; 1.
PROSITE; PS00225; IGF_EINDING; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS0184; VWFC_2; 1.
PROSITE; PS0104; VWFC_2; 1.
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HEPARIN-BINDING.
CTCK.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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CONNECTIVE IISSUE GROWTH FACTOR.
IGFBP.
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0ECF8470B357EA95 CRC64;
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/FTIG=VSP_002460.
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38069 MW;
          InterPro; IPR000884; TSP1.
InterPro; IPR01007; VWF_C.
Pfam; PF00107; Cyg knot; 1.
Pfam; PF0019; IGFBP; 1.
Pfam; PF00099; tsp_1; 1.
Pfam; PF00099; vwc; 1.
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349 AA;
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Best Local Similarity
Matches 176; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEPARIN-BINDING, AND CELL ADHESION.

MEDINE=2245756; Pubmed=12553876;

A MEDINE=2245756; Pubmed=12553876;

Ball D.K., Rachfal A.W., Kemper S.A., Brigstock D.R.;

Ball D.K., Rachfal A.W., Kemper S.A., Brigstock D.R.;

T factor (CTGF) containing module 4 alone stimulates cell adhesion.";

L J. Endocrinol. 176:R1-R7(2003).

-!- FUNCTION: Major connective tissue mitoattractant secreted by vascular endochelial cells. Promotes proliferation and divalent cation-dependent cell adhesion in many cell types including fibroblasts, myofibroblasts, endochelial and epithelial cells.

Enhances fibroblast growth factor-induced DNA synthesis.

-!- SUBGNILT: Monomer.

-!- SUBCELLUTAR LOCATION: Found in the extracellular matrix and as a soluble form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=1; Synonyms=Long;
Isold=29279-1; Sequence=Displayed;
Name=2; Synonyms-Short; Sequence=VSP_002460;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the CCN family.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 TVSP type-1 domain.
-!- SIMILARITY: Contains 1 TVSP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Chondrocytes;
MEDLINE=20080284; PubMed=10614647;
Makanishi T., Nishida T., Shimo T.,
Tamatani T., Tezuka K., Takigawa M.;
Tamatani T., Tezuka K., Takigawa M.;
"Effects of CTGF/Hcg24, a product of a hypertrophic chondrocytespecific gene, on the proliferation and differentiation of
TISSUE=Aorta;
MEDLINE=97207446; PubMed=9054739;
MEDLINE=97207446; PubMed=9054739;
Oemar B.S., Werner A., Garnier J.M., Do D.D., Godoy N., Nauck M.
Marz W., Rupp J., Pech M., Luescher T.F.;
"Human connective tissue growth factor is expressed in advanced atherosclerotic lesions.";
Circulation 95:831-839(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121009; -. Gextracellular matrix; TAS. GO:0005586; C:extracellular matrix; TAS. GO:0005886; C:plasma membrane; TAS. GO:0005820; F:insulin-like growth factor binding; TAS. GO:000851; P:cell growth and/or maintenance; TAS. GO:0008541; P:cell growth and/or maintenance; TAS. GO:0008541; P:response to wounding; TAS.
                                                                                                                                                                                                                                                                                                       Cobley V.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR006207; Cys knot C.
InterPro; IPR000867; Insl_gro_fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific gene, on the proliferati
chondrocytes in culture.";
Endocrinology 141:264-273(2000).
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PIR; A40551; A40551.
Genew; HGNC:2500; CTGF.
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SEQUENCE FROM N.A.
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A Mathans M., Schwitters C., Hove M., Rupp S., Erondu N.E.;

TISSUE—Liver;

Thromosomal gene and demonstration of promoter activity.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: Major connective tissue mitoattractant secreted by vascular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediates heparinced and divalent cation-dependent cell adhesion in many cell types including fibroblasts, myclibroblasts, endothelial and epithelial cells (By similarity). Enhances fibroblast growth factor-induced CC orluble form (By similarity).

- SUBGNIT: Monomer (By similarity).

- SUBGNIT: Monomer (By similarity).

- SUBGNIT: Monomer (By similarity).

- SUBGNIT: Contains 1 (GFBP domain.

- SIMILARITY: Contains 1 (GFBP domain.

- SIMILARITY: Contains 1 TSP type-1 domain.

- SIMILARITY: Contains 1 TSP type-1 domain.
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PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS00222; IGF EINDING; 1.
PROSITE; PS00221; TSP! 1.
PROSITE; PS0108; VWFC 1; 1.
PROSITE; PS01108; VWFC 2; 1.
PROSITE; PS01108; VWFC 2; 1.
CE11 adhesion; DNA synthesis; Extracellular matrix; Heparin-binding; Signal. 1 26 POTENTIAL.
CHAIN 27 349 CONNECTIVE TISSUE GROWTH FACTOR.
                                                                                 Bos taurus (Bovine).
Sukaryota: Metazora; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                          Lillensiek B., Lin Z., Fotsis T., Schimanski M., Bierhaus A., Kanitz M., Kauffmann G., Schweigerer L., Ziegler R., Nawroth P.P.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
O18739; Q9GL71;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Connective Lissue growth factor precursor.
CTGF OR CCN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF000137; AAB66596.1; -
EMBL; AF309555; AAG30290.1; -
INTERPRO; IPR006209; Cyg knot.
INTERPRO; IPR000807; Cyg knot.
INTERPRO; IPR000807; ISPI.
INTERPRO; IPR000807; ISPI.
INTERPRO; IPR001007; VWF C.
Pfam; PF00207; Cyg knot; 1.
Pfam; PF00209; tsp. 1; 1.
Pfam; PF00009; tsp. 1; 1.
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SMART, SM00121; IB; 1.
SMART, SM00209; TSP1; .
SMART; SM00214; VWC; 1
                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                     NCBI TaxID=9913,
                                                                                                                                                                                TISSUE=Aorta;
Liliensiek B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 TEWSACSKTCGMGISTRVINDNAFCRLEKQSRLCWVRPCEADLEENIKKGKKCIRTPKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 CKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 DDQDDLLGLDASEVELTRNNELIAIGKG-SSLKRLPVFGTEPRVLFNPLHAHGQKÇIVQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 TSWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKWRFRCEDGEMFSKNVMMIQSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSSSTFRTLAVAVTLIHLTRLALST-----CPAACHCPL-EAPKCAPGVGLVRDGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSATGLGPVRCAFVLL --- LALCSRPASSQDCSAPCOCPAGPAPRCPAGVSLVLDGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-UU-1998 (Rel. 36, Created)
15-UU-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Connective tissue growth factor precursor.
CTGF OR CCN2.
Sus scored (Pig)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97390475; PubMed=9242708;
Brigstock D.R., Steffen C.L., Kim G.Y., Vegunta R.K., Diehl J.R.,
Harding P.A.;
                            TSP TYPE-1.
HEPARIN-BINDING (BY SIMILARITY).
CTCK.
BY SIMILARITY.
CO -> DC (IN REF. 1).
A -> T (IN REF. 1).
CUPP -> SEDE (IN REF. 1).
CUPP -> YI (IN REF. 1).
CDEP -> SEDE (IN REF. 1).
CD -> Q (IN REF. 1).
C -> Y (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                  44.6%; Score 937; DB 1; Length 344.7%; Pred. No. 8.5e-66; ive 65; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 KCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 ACHYNCPGDNDIFESLYYRKMYGDM 348
                                                                                                                                                                                                                                                                                                                                                                 37924 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.7
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
209
269
284
349 AA;
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"Purification and characterization of novel heparin-binding growth factors in uterine secretory fluids. Identification as heparin-
Education uterine secretory fluids. Identification as heparin-
Education uterine secretory fluids. Identification as heparin-
Education of connective tissue growth factor.";

"PUNCTION: Major connective tissue mitoattractant secreted by vascular endothelial cells. Promotes proliferation and differentiation of chondrocytes (By similarity). Mediates heparin-
and divalent cation-dependent cell adhesion in many cell types including fibroblasts, myclibroblasts, endothelial and epithelial cells (By similarity). Enhances fibroblast growth factor-induced DNA synthesis (By similarity).

"SUBJUNIT: Monomer (By similarity).

"SUBJUNIT: Monomer (By similarity).

"SUBJUNIT: Monomer (By similarity).

"STMILARITY: Contains I IGPBP domain.

"SIMILARITY: Contains I IGPBP domain.

"SIMILARITY: Contains I TSP type-1 domain.

"SIMILARITY: Contains I TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSSSTRTLAVAVTLLHLTRLALSTCPAA-----CHCPL-EAPKCAPGVGLVRDGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; P80118; CTCK 1; 1.
PROSITE; P801225; CTCK 2; 1.
PROSITE; P800222; IGF BINDING; 1.
PROSITE; P550092; TSP1; 1.
PROSITE; P5501208; VWFC 2; 1.
PROSITE; P550184; VWFC 2; 1.
Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWFC.
HEPARIN-BINDING (BY SIMILARITY).
CTCK.
BY SIMILARITY.
WY BESIOE2B252D4A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CONNECTIVE TISSUE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.7%; Score 919; DB 1; Length 349
44.9%; Pred. No. 2.1e-64;
ive 62; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR001007; WPP.C.
Pfam; PF00209; Cys knot; 1.
Pfam; PF00209; IGFBP; 1.
Pfam; PF00099; tsp_l; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
349
H 330
293
307
323
325
325
B 325
B 38007 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U83916; AAC48756.1; -.
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Best Local Similarity 44.9<sup>3</sup>
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00041; CT; 1.
SMART; SM00121; IB; 1.
SMART; SM00209; TSP1; 1
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
287
292
349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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53 CKVCAKQINEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGES 112

MSATGLSPVRCAFVLL - - - LALCSRPASGODCSGOCQCAAGKRRACPAGVSLVLDGCGC

원 장

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CONTOCT V., MATTINETIE C., Dambrine G., Plassiart G., Brisac M.,
A Crochet J., Perbal B.,
Crochet J., Perbal B.,
The Coll in myeloblastomis-associated virus type 1-induced
The phroblastomas.";
Mol. Cell. Biol. 12:10-21(1992)
THORITON: INMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
CROWTH REGULATION: ITS OVEREXPRESSION IS ASSOCIATED WITH
TUMORIGARESIS AND EXPERSSION OF A N-TERMINAL-TRUNCATED VERSION
CON TOWN GENE IN CHICKEN EMBRYONIC PIBROBLAGYS (GEP) IS SUFFICIENT
CONDUCE THE TRANSFORMATION OF CEF IN VITRO.
TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.
TO SUBJECTIVILAR LOCATION: Secreted.
TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN AND SPLEEN IN ADULT CHICKEN.
CONTRACTOR OF THE TRANSFORMATION IS NORMALLY ARRESTED IN ADULT CHICKEN.
CONTRACTOR OF THE TRANSCRIPTION IS NORMALLY ARRESTED IN ADULT TINDUCED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
|::||||| | |:: ||| || || |:||: CRLCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK-DGAPCVFGGTVYRSGES 115
                                                             POPNCKHOCTCIDGAVGCIPLCPQELSIPNLGCPNPRLVKVSGQCCEEWYCDEDSIKDSL 172
                                                                                                                                                                                                                                                                                   TEWSACSKTCGMGISTRVTNDNAPCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIS 263
                                                                                                                                                                                                                                                                                                                                                            264 KPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVBFKCPDGEVMKKSMMFIKTC 323
                                                                                                                                                                                             173 ------RANCLVQFALAAYRLEDTFGPDFTMM-----RANCLVQT 203
                                                                                                                                                                                                                                             TSWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSP 291
                                                                                                                                                                                                                                                                                                                                292 EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSC 351
                                                                                            -!- SIMILARITY: Belongs to the CCN family.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 VMFC domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                   173 DDQDDLLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OT7-2003 (Rel. 42, Last annotation update)
10-OT7-2003 (Rel. 42, Last annotation update)
NOV protein precursor (Nephroblastoma overexpressed gene protein).
NOV OR CCM3.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRALIBEROWN LOGHORD;
MEDILINE=92107157; Pubmed=1309586;
Joliot V., Martinerie C., Dambrine G., Plassiart G., Brisac M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     352 KCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 ACHYNCPGDNDIFESLYYRWYGDM 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                     204
                     5,
                                                                113
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                                                                                                                                                                                                           Weiskirchen R., Bister K.;
Submitted (AuG-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Immediate-early protein likely to play a role in cell
growth regulation (By similarity).

-!- SUBCELLUININ: Secreted (By similarity).

-!- SIMILARITY: Belongs to the CCN family.

-!- SIMILARITY: Contains 1 IGFBP domain.

-!- SIMILARITY: Contains 1 TSP type-1 domain.

-!- SIMILARITY: Contains 1 TSP type-1 domain.

-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
NOV protein precursor (Nephroblastoma overexpressed gene protein)
NOV OR CCN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TARET.

TSP TYPE-1.

CTCK.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.7%; Score 856; DB 1; Length 35
Best Local Similarity 43.6%; Pred. No. 1.7e-59;
Matches 163; Conservative 47; Mismatches 108; Indels
                                                                                                 Coturnix coturnix japonica (Japanese quail)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r; Signal.
POTENTIAL.
NOV PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U13063; AAA21128.1; ...
InterPro; IPR006209; Cys knot.
InterPro; IPR006207; Cys_knot.
InterPro; IPR000864; TSP1.
InterPro; IPR000864; TSP1.
InterPro; IPR0000864; TSP1.
InterPro; IPR000007; VWF_C.
Pfam; PP00007; Cys_Knot; 1.
Pfam; PP00090; LSP_1; 1.
Pfam; PP00090; LSP_1; 1.
Pfam; PP00090; LSP_1; 1.
SWART; SM00121; IS; 1.
SWART; SM00121; IS; 1.
SWART; SM00212; ISP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; IGF EINDING; 1.
PROSITE; PS01208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 N
38667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 AA;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                           NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proto-oncogene;
SIGNAL 1
CHAIN 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 ESCSPILPCDESGGLYCDRGPEDGGGAGICMV-LEGDNCVFDGMIYRNGETFQPSCKYQC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCD-EDSI-----KDSLDDQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 DDLLGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 BATLGIDVSD-----SSANCIECTIEWS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 ACSKSCGMGFSTRVTURNQQCEMVKQTRLCMMRPCENEEPSD-KKGKKCIQTKKSMKAVR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 FEYKNCTSVQTYKPRYCGLCNDGRCCTPHNTKTIQVEFRCPQGKFLKKPMMLINTCVCHG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 BDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 QCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKWRFRCEDGEMFSKWVMMIQSCKCNY 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LAVAVTLIHLTRLA----LSTCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   VWFC.

TSP TYPE-1.

CTCK.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

40.9%; Score 861; DB 1; Length 351
Best Local Similarity 44.5%; Pred. No. 6.9e-60;
Matches 165; Conservative 44; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                      NOV PROTEIN. IGFBP.
                                     InterPro; 1PR006208; Cy8 knot.
InterPro; 1PR006207; Cy8_knot.
InterPro; 1PR000807; TunE gro_fac_pr
InterPro; 1PR000804; TSP1.
InterPro; 1PR000804; TSP1.
InterPro; 1PR001007; VWF.C.
Pfam; PF000107; Cy8_knot; 1.
Pfam; PF000107; Cy8_knot; 1.
Pfam; PF000107; Cy8_li 1.
Pfam; PF000107; Cy8_li 1.
SWART; SW00011; ISP, 1.
SWART; SW0011; ISP, 1.
SWART; SW0011; ISP, 1.
SWART; SW0011; ISP, 1.
SWART; SW0011; ISP, 1.
PROSITE; PS01125; CTCK, 1.
PROSITE; PS01125; CTCK, 1.
PROSITE; PS011208; VWC, 1.
PROSITE; PS01108; CTCK, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 NCPOSNNAFFQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 2
351 AA;
                                                                                                                                                                                                                                                                                                                                                     Proto-oncogene;
SIGNAL 1
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ID NOV_COTJA
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TISSUESEXEN,

X MEDLINES238827; PubMed=12477932;

KRDLINES238827; PubMed=124, Grouse L.H. Schaefer C.F., Bark N.K.,

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Rhitting M., Touchman J.W., Green E.D., Dickson M.C.,
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                                                                                                119 HQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCD-EDSI----KDSL 172
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SLPVILLLLLLLLLRPSEVNGREAPCPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCAR 67
                                                                 QLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCK
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MEDLINE=94336229; PubMed=7520150;
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MARTHINETIE C., Huff V., Joubert I., Badzioch M., Saunders G.F.,
Strong L.C., Perbal B.;
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Productions No. Cerumond. N. Schmitt. 1. Warrant M. M. Schler U., Smalle D. E., R. Butterfald Y. S. M., Krzyvinski Mt., Skalke U., Smalle D. E., Schmerch A., Schein J. E., Jones S. J. M., Marza M. M. Marza M. M. Schmerch A., Schein J. E., Schein J. Schein J. E., Schein J. Schein J. E., Schein J. E., Schein J. E., Schein J. Schein J. E.,
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SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
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TSP TYPE-1.
CTCK.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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NOV PROTEIN HOMOLOG.
IGFBP.
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InterPro; IPR006209; Cys Knot.
InterPro; IPR006209; Cys Knot.
InterPro; IPR00867; Insl_gro_fac_pr
InterPro; IPR000867; Insl_gro_fac_pr
InterPro; IPR000867; VWF.C.
Pfan; PF00109; VYS Knot; 1.
Pfan; PF00009; IGFB; 1.
Pfan; PF00009; TSP1; 1.
SWART; SW00119; IGFB; 1.
SWART; SW00119; ISP; 1.
SWART; SW00119; ISP; 1.
SWART; SW00219; VWC; 1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; IGF BINDING; 1.
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Matches 158; Conservat
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
NOV protein homolog precursor (NovH) (Nephroblastoma overexpressed gene protein homolog).
NOV OR CCN3.
    BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

N -> K (IN REF. 3).

035D5BF4576BD85B CRC64;
                                                                                                                                       DB 1; Length 357;
                                                                                                                                       39.9%; Score 839.5; DB 1; Length 43.8%; Pred. No. 3.3e-58; ive 52; Mismatches 116; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Interacts with FBLN1 (By similar SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Belongs to the CCN family.
-!- SIMILARITY: Contains 1 UGFB domain.
-!- SIMILARITY: Contains 1 VFC domain.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
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    333 B)
337 B)
97 N-
280 N-
97 N-
39162 MW;
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Matches 163; Conservative
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357 AA;
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DISULFID
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CARBOHYD
CONFLICT
SEQUENCE
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SIGNAL
REPUBLICE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=C57EL/6J; TISSUE=Embryonic head, and Spinal cord;

MEDINE=C57EL/6J; TISSUE=Embryonic head, and Spinal cord;

RA MIRAIGO I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA MIRAIGO I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA MIRAIGO I., Osato N., Hasegawa Y., Nogami A., Schonbach J.,

RA Baldarelli R., Manapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Balte J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Balte J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Balte J.A., Rawali H., Kawaswa Y., Nedzierski R., King B.L.,

Ranai A., Kawaji H., Kawaswa Y., Kedzierski R., King B.L.,

Ranai A., Kawaji H., Kawaswa Y., Kedzierski R., Ving B.L.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Magabina T., Numata K., Okido T., Param W.J., Pertea G., Pescle G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Secou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teaddale R.D., Tomita M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teaddale R.D., Tomita M.,

RA Wilming L.G., Wynshaw-Boris A., Vanagisawa M., Yang I., Yang I.,

Hara A., Hashizume W., Imcrani K., Ishii Y., Itoh M., Kagawa I.,

RA Minaiyais of the mouse transcriptome based on functional annotation of R. Nature 420:563-573(2002).

RA Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Breast tumor; STRAIN=Cacch II, TISSUE=Breast tumor; STRAIN=Cacch II, TISSUE=Breast tumor; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Attaubner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-1929'SV, and ICR; TISSUE-Brain;
MEDLINE-9713123; PubMed-8975721;
Snaith M.R., Natarajan D., Taylor L.B., Choi C.P., Martinerie C.,
Snaith M.R., Schoffield P.N., Boulter C.A.;
"Genomic structure and chromosomal mapping of the mouse nov gene.";
Genomics 38:425-428(1996).
                                            NOV MOUSE STANDARD; PRT; 354 AA.

664299; Q8CA67;

10.1NOV-1997 (Rel. 35, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
NOV proctein homolog precursor (NovH) (Nephroblastoma overexpressed gene proctein homolog).
                                                                                                                                   NOV OŘ CCN3.

Mus musculus (Mouse).

Eukarycia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS7BL/6;
STRAIN=CS7BL/6;
SPEAGO OS; PubMed=8622864;
Martinerie C., Chevalier G., Rauscher F.J. III, Perbal B.;
"Regulation of nov by WT1: a potential role for nov in
                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 12:1479-1492(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                         nephrogenesis.";
                               RESULT 14
NOV MOUSE
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Parachemical, Warneline K., Daniel M.P., Robins M.P., Robins T. L., Scheer T. E., Baronscan M. L., Warneline K., Daniel M.P., Robins M. Carring C., Millah S. G., Loquellano N.A., Peters G.J., Maid S. J., Congellano N.A., Peters G.J., Maid S. J., Maid J.,
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us-09-495-448a-2.rsp

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or send an email to license@isb-sib.ch)
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Best Local Similarity
Matches 152; Conserv
                                                                                                                                                                                                                                                                                                                               343 AA;
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                                                                                                                        LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGOKCIVQTTSWSQCSKS 240
                                                                                                                                                                                                  63 DCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCT 122
                                                                                                                                                   CIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVC--DEDSIKDSLDDQDDLLG 180
                                                                                                                                                                                                                           CGTGISTRVTNDNPECRLVKETRICEVRPCGQ-PVYSSLKKGKKCSKTKKSPEPVRFTYA 299
                                                                                                                                                                                                                                                                GCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPH 359
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                                                                          7 RTLAVAVTLLH-LTRLALS-TCPAAC--HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNE 62
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
N-LINKED (GLCNAC. . ) (POTENTIAL)
R -> G (IN REF. 3; BAC30363)
08ECE8CFC67829DE CRC64;
                                                        38;
                                      Length 354;
                                     Query Match
39.3%; Score 827; DB 1; Length 35
Best Local Similarity 44.2%; Pred. No. 3.1e-57;
Matches 161; Conservative 51; Mismatches 114; Indels
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
NOV protein homolog precursor (Xnov).
                                                                                                                                                                                                                                                                                                                                                                    343 AA
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MEDLINE=96257227; PubMed=8666280;
Ying Z., King M.L.;
         6 6 6
354 AA; 38928 MW;
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                    360 PNEA 363
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PS1609;
 CARBOHYD
CONFLICT
SEQUENCE
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343 NOV PROTEIN HOMOLOG.

159 VWFC.

235 TSP TYPE-1.

236 BY SIMILARITY.

340 BY SIMILARITY.

316 BY SIMILARITY.

318 BY SIMILARITY.

318 BY SIMILARITY.

318 BY SIMILARITY.

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EMBL, U37063; AAB17096.1; -..
InterPro; IPR006209; Cy8 knot.
InterPro; IPR006207; Cy8 knot.
InterPro; IPR000864; Insl_gro_fac_pr.
InterPro; IPR000864; ITSI.
InterPro; IPR000864; TSI.
InterPro; IPR000007; VWF_C.
Pfam; PP00020; LSP_1; 1.
Pfam; PP000209; LSP_1; 1.
Pfam; PP00090; LSP_1; 1.
Pfam; PP00090; LSP_1; 1.
SMART; SM00121; IB1; 1.
SMART; SM00121; IB1; 1.
SMART; SM00121; IB1; 1.
SMART; SM00121; IB1; 1.
PROSITE; PS01185; CTCK_2; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01229; TSP_1; 1.
PROSITE; PS01229; UNFC_1; 1.
PROSITE; PS01208; WNFC_1; 1.
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Ogvyk3 drosophila
Ogwyk7 homo sapien
Ogdf21 scyliorhinu
Ogdf21 scyliorhinu
Ogdf21 scyliorhinu
Ogdf21 scyliorhinu
Ogdf23 cenorhabdi
Og8536 ceenorhabdi
Og737 ceenorhabdi
Og737 ceenorhabdi
Og737 gallus gall
Og0x43 gallus gall
Og0x44 gallus gall
Og1x44 gallus gall
Og7574 bos taurus
Og7575 mus musculu
Og6cg65 mus musculu
Og8cg65 mus musculu

us-09-495-448a-2.rspt

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CYR61.
Rattus norvegious (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SIGNIENCE FROM N.A.

SIGNIENCE FROM N.A.

DIGGAL H., YOREKUTE H., FUTUKAWA K., YAMAMOCO H.;

UDOKI H., YOREKUTE H., FUTUKAWA K., YAMAMOCO H.;

SUDMITTED (JUN-1998) to the EMBL/GenBank/DDBJ databases.

REMEL, ABUISAN'; BAA7339.1, -..

ROJ; GO:0005576; C:extracellular; IEA.

GO; GO:000558; P:insulin-like growth factor binding; IEA.

ROJ; GO:0005589; P:regulation of cell growth; IEA.

RITHERPRO; IPRO06207; Cys_knot.C.

RITHERPRO; IPRO06207; Cys_knot.C.

RITHERPRO; IPRO01091; VWP.C.

RITHERPRO; IPRO01007; VWP.C.

REMIN PRO0019; IGFEP; 1.

REMIN PRO0009; IGFEP; 1.

REMIN PRO0009; IGFEP; 1.

REMIN PRO0009; VWP. 1.

REMIN PRO0009; VWP. 1.
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Last annotation update)
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                                                                     Q91BG7
Q86XX4
Q8T3A6
Q9XWD6
Q90Z43
Q90X44
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Q8VEA6
Q964N4
Q21281
Q9JLL0
Q8CG65
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Q9NZV1
Q86AK7
Q9VVK3
Q8WYK7
Q9UDE4
Q9DF21
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SWART; SM00121; IB; 1.
SWART; SM00209; TSP1; 1.
SWART; SM00214; VWC; 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01222; IGF_EINDING; 1.
                                                                                                                                                                                                                   035888
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                                                                                                                              PRELIMINARY;
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Q9WTM9
     A COCCOS ON THE 
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Q98tx5 xenopus lae
Q9uid7 homo sapien
Q98tq8 gallus gall
Q42607 xenopus lae
Q9pt8 notophthalm
O37765 sus scrofa
O95958 homo sapien
Q9500 rattus norv
Q862t0 hos taurus
Q82t6 tattus norv
Q81v29 mus musculu
Q91v29 mus spicile
Q91v40 drosophila
                                                                                                                              April 22, 2004, 17:53:04; Search time 38.3987 Seconds (without alignments) 3114.206 Million cell updates/sec
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                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9WTM5
Q9WTD7
Q9BTQ8
Q9SPTB0
Q97765
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Q9FSC0
Q9R2C0
Q9R2
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sp archea:*
sp_bacteria:*
sp_bungi:*
sp_human:*
sp_invertebrate:*
sp_mhc:*
sp_organelle:*
sp_organelle:*
sp_rodent:*
sp_rodent:*
sp_vortebrate:*
sp_vortebrate:*
sp_wortebrate:*
sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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113
113
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Match Length DB
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Maximum DB :
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68 68 184

241 238

us-09-495-448a-2.rspt

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69 PCDHTKGLECNFGASSRAIKGICRAKSEGRPCEYNSKIYQNGESFQPNCKHQCTCIDGAV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 SSVKKYRPRYCGSCVDGRCCTPQQTRTVKIRFRCEDGETFTKNVMMIQSCRCNYNCPHIN 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGISTRVTNDNPECRLVKETRICEVRPCGOPVYSSLKKGKKCSKTKKSPEPVRFTYAGC 301
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                                                                                                                                                                                                                                                                                                                                                                        69 PCDHIKGLECNFGASSIALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 GCIPLCPQELSLPNIGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDL----LGLDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVELTRINELIAIGKGSSLKRLPVFGTEPRVLFNPLHAH---GOKCIVOTTSWSOCSKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPN
                                                                                                                                                                                                                                                                                             9 LAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQ
                                                                                                                                                                                                                                                                                                                       10 LAIAL-LSGFIDLAVSSCPAVCQCPVEVPKCAPGVGLVLDGCGCCCKICAKQLNEDCSKTH
                                                                                                                                                                                                                                                         19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P SEQUENCE OF 1-107 FROM N.A.

TISSUE=Kidney;

A Anding B., Long Y.;

Toloning of a new gene down-regulated in the small-cell tumor embryonal-rhabdomyosarcoma (RMS).";

Submitted (MAY-1997) to the EWBL/GenBank/DDBJ databases.

I Submitted (MAY-1997) to the EWBL/GenBank/DDBJ databases.

R GO; GO:0005520; F:insulin-like growth factor binding; IEA.

R GO; GO:0005520; F:insulin-like growth factor binding; IEA.

R GO; GO:0005520; F:insulin-like growth factor binding; IEA.

R GO; GO:0005520; F:insulin-like growth; IEA.

R InterPro; IPR006209; Cye knot.

R InterPro; IPR000867; InsI_gro_fac_pr.

R InterPro; IPR000884; IPRI_GFO_Fac_pr.

R InterPro; IPR000894; IPRI_GFO_Fac_pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                     13; Length 375;
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Mammalia; Butheria; Primatee; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                Query Match

77.2%; Score 1624.5; DB 13; Lengt
Best Local Similarity 77.5%; Pred. No. 2.1e-146;
Matches 293; Conservative 29; Mismatches 37; Indels
SWART; SM00121; IB; 1.
SWART; SM01209; TSP1; 1.
PROSITE; P801216; VTCK, 1; 1.
PROSITE; P801225; CTCK, 2; 1.
PROSITE; P801225; CTCK, 2; 1.
PROSITE; P801227; IGF BINDING; 1.
PROSITE; P801022; TSP1; 1.
PROSITE; P801046; VWFC, 2; 1.
SEQUENCE 375 AA; 41460 MW; 78075CA7B380304E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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EA-YPYYRLFNDIHKFRD 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EASFRLYSLFNDIHKFRD 379
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
CYR61 protein.
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Q9UID7
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHGOKCIVQTTSWSQCSKS
                                                                                                                                                                                                                                            1 MSSSTFRTLAVAVTLIHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
                                                                                                                                                                                                    Gaps
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Q1-UJN-2001 (TrEMBLrel. 17, Last sequence update)

01-UJN-2001 (TrEMBLrel. 17, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Secreted cysteine-rich protein cyrél.

Xenopus laevis (African clawed frog).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Latinkic B.V., Benett B., Smith J.C.;
Latinkic B.V., Benett B., Smith J.C.;
Characterization of Xenopus cyfel.";
Characterization of Xenopus cyfel.";
Characterization of the EMBL/GenBank/DDBJ databases.
E Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
E GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
R GO; GO:000558; P:regulation of cell growth; IEA.
R GO; GO:000558; P:regulation of cell growth; IEA.
R InterPro; IPR006209; Cyg Mrot. C.
R InterPro; IPR000867; Inal_gro_fac_pr.
R InterPro; IPR000087; Inal_gro_fac_pr.
R InterPro; IPR00107; VWF_C.
R Pfam; PF00007; Cyg Knot; I.
R Pfam; PF00009; tsp_l;
R Pfam; PF00009; tsp_l;
R Pfam; PF00009; tsp_l;
R Pfam; PF00099; tsp_l;
R Pfam; PF00099; tsp_l;
R Pfam; PF00099; Cyg Li I.
                                                                                                                                                           Query Match 98.7%; Score 2076; DB 11; Length 379; Best Local Similarity 98.2%; Pred. No. 2e-189; Matches 372; Conservative 4; Mismatches 3; Indels 0
                                                                                1 24 POTENTIAL.
25 379 CYR61.
379 AA, 41728 MW; D2ABAFD77B84762B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 AA.
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  PS50092; TSP1; 1.
PS01208; VWFC_1; 1.
PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
    PROSITE; PROSITE; PROSITE; Signal.
                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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Q98TX5
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245 ISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCSSV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 ISTRVTNDNAFCRLEKQSRLCMVRPCBADLEENIKKGKKCIRTPKISKPIKFELSGCTSV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 KKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEAS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 GAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLGLDASE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIAVALLLALIGPEVRGQECSGQCCCGSGPGPSCPAGVSLVLDGCGCCRVCAKQLGELCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 KTOPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYONGESFOPNCKHOCTCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 VELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGOKCIVQTTSWSQCSKSCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GAVGCVPLCSMDVRLPSPDCPYPRRVKLPGKCCEEWVCDE--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TLAVAVTLIHL-TRLALSTCPAACHCPL-EAPKCAPGVGLVRDGCGCCKVCAKQLNEDCS
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (Arican clawed frog).
Xenopus laevis (African clawed frog).
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                       SIĞNAL 1 21 POTENTIAL.
CHAIN 22 344 CONNECTIVE TISSUE GROWTH FACTOR.
SEQUENCE 344 AA; 37499 MW; 69E639AF69BF1D00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.7%; Pred. No. 5.2e-81;
Matches 170; Conservative 61; Mismatches 103; Indels 38
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U45524; AAB67639.1; -.
EMBL, U43523; AAB67639.1; -.
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                      Pfam; PF00007; Cya knot; 1.
Pfam; PF000019; Gya knot; 1.
Pfam; PF000091; tsp_1; 1.
Pfam; PF00093; vwc; 1.
SWART; SW00041; CT; 1.
SWART; SW00209; TSP1; 1.
SWART; SW00209; TSP1; 1.
SWART; SW00209; TSP1; 1.
PROSITE; PS01125; CTCK 1; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS00225; TSP 1; 1.
PROSITE; PS00202; TSP1; 1.
PROSITE; PS00202; TSP1; 1.
PROSITE; PS01081; VWFC 1; 1.
PROSITE; PS01084; VWFC 2; 1.
7; VWF_C.
_knot; 1.
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NCBI_TaxID=8355;
  InterPro; IPR001007;
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                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OKCIVOTISWSĄCSKICGIGISIRVINDNPECRLVKEIRICEVRPCGOPVYSSLKKGKKC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 GCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 NGESFOPNCKHOCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSGQCCEEWVCDEDSI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XDSLDDQDDL----LGLDASEVELTRNNELIAIGKGSSLKRLPVFGTEPRVLFNPLHAHG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OKCIVOTISMSQCSKSCGTGISTRVINDNPECRLVKETRICEVRPCGQPVYSSLKKGKKC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKIKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGRCCIPLQIRIVKWRFRCED---- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 SKITKKSPEPVRFIYAGCLSVKKYRPKYCGSCVDGRCCTPOLIRI-----CEDAVPLRRW 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GCGTHPNLCIHLGHTASPISYKHHTKGLECNFGASSTALKGICKAQSEGRPCEYNSKIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.2%; Score 1455; DB 4; Length 334;
Best Local Similarity 78.9%; Pred. No. 2.6e-130;
Matches 273; Conservative 13; Mismatches 32; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEMFSKN----VMMIQSCKCNYNCPHPNEASFRLYSLFNDIHKFRD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 GDIFQERHDDPVL----KCNYNCPHANEAAFPFYRLFNDIHKFRD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF463517; AL68834.1; -...
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005520; F:insulin-like growth factor binding; IEA.
GO; GO:0001558; P:regulation of cell growth; IEA.
InterPro; IPR006208; Cys_knot.
InterPro; IPR006209; Cys_knot.
InterPro; IPR00637; INSI
InterPro; IPR00847; ISBL
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Mukudai Y., Kubota S., Takigawa M.;
Submitred (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ298335; CAC33438.1;
EMBL; AF463517; AAL68834.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Gygi D., Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                               9188987A7352E948 CRC64;
                                                Pram; Pro0000; tsp_1; 1.
Pram; Pro0009; tsp_1; 1.
SMART; SM00041; CT; 1.
SMART; SM00209; TSP1; 1.
PROSITE; SM00214; VWC; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01209; TSP1; 1.
PROSITE; PS01209; WWC; 2; 1.
PROSITE; PS01209; VWFC; 1; 1.
PROSITE; PS0184; VWFC; 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
     Pfam; PF00007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
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129 GCIPLOPQELSIPNIGCPNPRLVKVSGQCCEEWYCDEDSIKDSLDDQDDLLGLDASEVEL 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LAVAVTLLHLTRLALSTCPAACHCPLBAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 PCDHTKGLECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 TRNNELIAI-----GKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRVGPALAVYRQBETYGPDSSLMR-------ANCLVQTTEWSACSKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GTGISTRVTNDNPBCRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 347;
              Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00222; TGF ENNDING; 1.
PROSITE; PS50092; TSPI; 1.
PROSITE; PS510208; VWFC_2; 1.
PROSITE; PS50184; VWFC_2; 1.
SEQUENCE 347 AA; 38098 MW; 38782399F27672C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Connective tissue growth factor.
CTGF.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
43.8%; Score 920.5; DB 13;
Best Local Similarity 45.1%; Pred. No. 2.4e-79;
Matches 169; Conservative 54; Mismatches 103;
MEDLINE=99033008; PubMed=9813273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 EASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIFESMYTRAMYGDM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
097765
AC 097765;
DT 01-MAY-1
DT 01-OCT-2
DE CONNECT-3
GN CTGF-3
OS SUS SUS
  SO DR REAL STREET STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLG--LDASEVELTRNNELIAIGKGSSL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 CNGECQCPNKVPVCDPGVRMVQDGCGCCKVCSKQLGELCTERDVCDPHKGLFCDFGSRVN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 RKIGVCTAR-EGAPCVFGGTVYRSGESFQSSCKYQCTCIDGGVGCVPLCSMDIRLPSPBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 ALKGICRAQSEGRPCEYNSRIYONGESFQPNCKHOCTCIDGAVGCIPLCPQELSLPNLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 KRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGISTRVTNDNPECRLVKETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRTATLPVEFKCPDGEVMKKNMMFIKTCACHFNCPGDNDIFEAMYYRKMYGDM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 LQTRIVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
Notophthalmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.6%; Score 937; DB 13; Length 343;
46.7%; Pred. No. 6.4e-81;
ive 60; Mismatches 90; Indels 3
F:insulin-like growth factor binding; IEA. P:regulation of cell growth; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gates P.B.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFPKRVKLPGKCCEEWVCDQ------PQERTLVGPALPAFRMEET
                                                                                                                                                                                                                                                                                      SWART; SW00041; CT; 1.
SWART; SW00121; IB; 1.
SWART; SW00129; TSP1; 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01185; CTCK 1; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01225; CTCK 2; 1.
PROSITE; PS01208; VWCC 2; 1.
SROUENCE 343 AA; 37966 MW; 93F221C5DB565A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Connective tissue growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Mismatches
                                                   InterPro; IPR006208; Cys_knot.
InterPro; IPR006207; Cys_knot.C.
InterPro; IPR000867; Insl_gro_fac.pr.
InterPro; IPR000084; TSP1.
InterPro; IPR001007; VWF.C.
Pfam; PF002107; Cys_knot; 1.
Pfam; PF002107; IGFBP; 1.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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TISSUE=Forelimb blastema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 46.74 Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Forelimb blastema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PT80
Q9PT80;
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86 RYETGVCACKSVG--CEFNQVHYHNGQVPQPNPLFSCLCVSGAIGCTP----LFIPKLA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 ALK-GICRAQSEGRPCEYNSRIYONGESFOPNCKHOCTCIDGAVGCIPLCPOELSLPNLG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CPAACHCPLEAPKCAPGYGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHWPCKCPQQKPRCPPGVSLVRDGCGCCKICAKQPGEICNEADLCDPHKGLYCDYSVDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGISTRVTNDNPECRLVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 SYXTMPAYRNLPLI.-----WKKKCLVQATKWTPCSRTCGMGISNRVTNENSNCEMRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 TRICEVRPCGQPVYSSLK--KGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CPNPRLVKVSGQCCEEWVCDEDSIXDSLDDQDDLLGLDASEVELTRNNELIAIGKGS
                                                                                                                                                                                                                   TISSUE=Mammary gland;
van Golen K.L., Davies S., Wu Z.F., Wang Y.F., Bucana C.D., Root H.
Chandrasekharapa S., Strawderman M., Ethier S.P., Merajver S.D.;
"A novel putative IGF-binding, tumor suppressor protein, LIBC, and
RhoC GTPase, are determinants of the inflammatory breast cancer
                                                                                                      Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                       Demotype."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, APL4379; AAD1151.1; EMBL/GenBank/DDBJ databases.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005589; P:insulin-like growth factor binding; IEA.

GO; GO:0005589; P:insulin-like growth; IEA.

R InterPro; IPR006209; Cys knot.

R InterPro; IPR006209; Cys knot.

R InterPro; IPR006849; Insl_gro_fac_pr.

R Pfam; PF00007; Cys knot; 1.

R Pfam; PF00009; IGFBp; 1.

R SWART; SW000219; IGFBp; 1.

R SWART; SW00229; ISFB; 1.

R PROSITE; PS01225; CTCK 2; 1.

R PROSITE; PS01225; TSP1; 1.

R PROSITE; PS01225; TSP1; 1.
                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 GSHCSGAK----GGKKSDQSNCSLEPLLQQL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTPLQTRIVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCIPNKSKMITIQFDCPNEGSFKWKMLWITSCVCQRNCREPGD
01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Lost in inflammatory breast cancer tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PSS6 PRELIMINARY; PRT; 176 AA. Q9PSS6; C1-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2000 (TrEMBLrel. 25, Last annotation update) Potential IGF binding protein (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.2%; Score 635.5; DB 4;
.larity 34.7%; Pred. No. 3.4e-52;
Conservative 57; Mismatches 116;
                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84448B
    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 FOPNCKHOCTCIDGAVGCIPLCPOELSLPNLGCPNPRLVKVSGQCCZEWVCDEDSIXDSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 DDQDDLLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPRVLFNPLHAHGQKCIVQT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 TEWSACSKTCGMGISTRVTNDNASCRIEKQSRICMVRPCEADLEENIKKGKKCIRTPKIS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 JSWSQCSKSCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPVRFTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSC 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSSSTFRTLAVAVTLLHLTRLALSTCPAA-----CHCPL-EAPKCAPGVGLVRDGCGC
                                                                                                             TISSUE-Uterus;
Harding P.A., Brigstock D.R.;
Harding and sequencing of a porcine connective tissue growth factor (CTGF) cDNA.";
CLOSIP, CDNA.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                          EMBL: U70066; AADOUT74.1: -

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:000558; P:insulin-like growth factor binding; IEA.

GO; GO:000558; P:insulin-like growth; IEA.

R GO; GO:000558; P:insulin-like growth; IEA.

InterPro; IPR006209; Cyg knot.

InterPro; IPR006809; Cyg knot.

InterPro; IPR000884; TSP1.

InterPro; IPR000884; TSP1.

R InterPro; IPR000884; TSP1.

R Pfam; PF00219; IGFEP; I.

R PR021TE; SM0024; WWC; I.

R PR021TE; PF0125; CTCK 2; I.

R PR051TE; PF0125; CTCK 2; I.

R PR051TE; PF0125; CTCK 2; I.

R PR051TE; PF01205; TSP1; I.

R PR051TE; PF01205; TSP1; I.

R PR051TE; PF01205; TSP1; I.

R PR051TE; PF01208; WWCC_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
42.4%; Score 891; DB 6; Length 34
Best Local Similarity 43.4%; Pred. No. 1.6e-76;
Matches 167; Conservative 65; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 ACHYNCPGDNDIFESLYYRKMYGDM 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 KCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                      SEQUENCE FROM N.A.
                                            NCBI_TaxID=9823;
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                                                    NON TER
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 PEDGGGAGIC----EGDNCVFDGMIYRNGETFQPSCKYQCTCRDGQIGCLPRCNLGLLLP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 NLGCPNPRLVKVSGQCCEEWVCDEDSIKDSLDDQDDLLGLDASEVELTRNNELIAIGKGS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AACPRPCGGRCPAEPPRCAPGVPAVLDGCGCCLVCARQRGESCSPLLPCDESGGLYCDRG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Jia J.D., Sedlaczek N., Bauer M., Wiecher D., Boigk G., Cho J.J.,
Jia J.D., Sedlaczek N., Enhypan D.;
Ruehl, M., Riecken E.O., Schuppan D.;
"Connective tissue growth factor is produced by hepatic stellate cells
and upregulated in rat liver fibrosis.";
Slumitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJS 6972; CAB41996.1; -.
InterPro; IPR001007; VWF_C.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                    24 STCPAAC - HCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKGLECNFG
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                        MEDINE=92096871; PubMed=1756408;
Martinerie C., Perbal B.;
"Expression of a gene encoding a novel potential IGF binding protein "Expression of a gene encoding a novel potential IGF binding protein in human tissues ";
C. R. Acad. Sci., III, Sci. Vie 313:345-351 (1991).
GO; GO:00055576; C:extracellular; IEA.
GO; GO:0005520; F:insulin-like growth factor binding; IEA.
GO; GO:0005520; F:insulin-like growth factor binding; IEA.
GO; GO:0001558; P:regulation of cell growth; IEA.
InterPro; IPR010867; Insl gro_fac_pr.
InterPro; IPR010121; IBs. 1.
SMART; SM00121; IBs. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GPDCPFPRKIEVPGECCEKWVC-----DPRDEVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 SLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGISTRVTNDN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 176;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
23.6%; Score 495.5; DB 13; Length
Best Local Similarity 41.4%; Pred. No. 3.6e-39;
Matches 96; Conservative 20; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                     18656 MW; 4FA69FFDB79B1C67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09R2C0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
Connective tissue growth factor (Fragment).
                                                                                                                                                                                                                                                    PROSITE; PS00222; IGF BINDING; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                     176 AA;
                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                NON TER
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SEQUENCE
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96 EGRPCEYNSRIYONGESFOPNCKHOCTCIDGAVGCIPLCPOELSLPNLGCPNPRLVKVSG 155
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WEDURNCE FROM N.A.

WEDURNCE PROM N.A.

WEDURNCE-25544902; PubMed=12658628;

MEDINE-25544902; PubMed=12658628;

MEDINE-25544902; PubMed=12658628;

MEDINE-25544902; PubMed=12658628;

MEDINE-25544902; MITAGARA A., Shiojima S., Ikawa H., Suzuki Y.,

Takahadhi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,

Takahadhi T., Imai K., Todoroki J., Hashizume K.;

Takahadhi T., Todoroki J., Hashizume K.;

Mol. Reprod. Dev. 65:9-18 (2003).

REDI, ABOSB999; BAS563891.;

Mol. Reprod. Dev. 65:9-18 (2003).

REDI, ABOSB999; BAS563891.;

REDI, ABOSB99; BAS563891.;

REDI, REDIO (1) CYB Knot. I.

PROSITE; SMORO1; CYB Knot. I.

PROSITE; PRO1185; CTCK.1; I.

PROSITE; PRO125; CTCK.2; I.

NON TER 125 125

SEQÜENCE 125 AA; 14352 MW; B6C7A27644DBFAE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 QCCEEWVCDEDSIKDSLDDQDDLLGLDASEVELTRNNELIAIGKGSSLKRL-PVFGTEPR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 NPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GVCTDGRCCTPHRTTTLPPVBFKCPDGEVMKKSMMFIKTCACHYNCPGDNDIFESLYYKKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 GSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEASFRLY--SL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DGAPCVFGGSVYRSGESFQSSCKYQCTCLDGAVGCVPLCSMDVRLPSPDCPFPRVKLPG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KDRTVVGPALAAYRLEDTFGPDPT 98
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                                                                                                                                                                                                                                                                                                                                                         Gaps
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Q1-UTNY-2003 (TrEMBLrel. 24, Created)
01-UTNY-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to connective tissue growth factor precursor (Fragment).
Similar to connective tissue growth factor precursor (Fragment).
Bost taurus (Bovine).
Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                              Query Match
17.8%; Score 374.5; DB 11; Length 128;
Best Local Similarity 43.3%; Pred. No. 8.5e-28;
Matches 68; Conservative 22; Mismatches 34; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 125;
                                                                                                                                                                     128 128 AA; 13803 MW; P30142D0C491B7C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 VLFNPLHAHGQKCIVQTTSWSQCSKSCGTGISTRVTN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM-----RANCLVQTTBWSACSKTCGMGISTRVTN 128
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46.8%; Pred. No. 1.2e-25;
ive 28; Mismatches 36;
Pfam; PF00093; vwc; 1.
SMART; SM0214; vwc; 1.
PS021TE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 KĊĊEĖWVĊDEP-----
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nes 58; Conserv
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260 KETRICEVRPCGOPVYSSLKKGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGR 319
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                                  Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.; "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 CCTPLQTRTVKMRFRCEDGEMFSKNVMMIQSCKCNYNCPHPNEASFRLY--SLFNDI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 KETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTYAGCSSVKKYRPKYCGSCVDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
                                                                                                                                                                          ENEL; AB039095; BAB68618.1; --
ENEL; AB039095; BAB68618.1; --
ENEL; AB039095; BAB68618.1; --
ENEL; AB039095; BAB68620.1; --
ENEL; AB039096; BAB68620.1; --
ENEL; AB039099; BAB68621.1; --
ENEL; AB039099; BAB68621.1; --
ENEL; AB039099; BAB68623.1; --
ENEL; AB039101; BAB68623.1; --
ENEL; AB039101; BAB68628.1; --
ENEL; AB039101; BAB68628.1; --
ENEL; AB039101; Cys knot.
InterPro; IPR006209; Cys knot.
Inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.3%; Score 343; DB 11; Length 1
48.7%; Pred. No. 7.9e-25;
ive 25; Mismatches 33; Indels
                                                                                                                                            (OCT-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 AA.
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                                                                                                                   Five Mus musculus subspecies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Conservative
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Best Local &
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Various strains;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
"Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Suppression subtractive hybridization identifies high glucose levels as a stimulus for expression of connective tissue growth factor and other genes in human mesangial cells.";

J. Biol. Chem. 274:8830-8834(1999).

EMBL; AF079531; AAD02838.1;

InterPro; IPR006208; Cyg.knot.

InterPro; IPR006209; Cyg.knot.

Pfam. PP00007; Cyg.knot.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=99150373; PubMed=10026205;
Murphy M., Godeon C., Cannon S., Kato S., Mackenzie H.S., Martin F.,
Brady H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIYRAKFCGVCIDGRCCIPHRITILIPVEFKCPHGEIMKKNMMFIKIC 107
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Kobayakawa H., Saitou N.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AA; 12767 MW; 23EA69FC0A60635E CRC64;
                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Connective tissue growth factor (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISP-12 protein (Fragment)
                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
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SEQUENCE FROM N.A.
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1091029
AC 09102
AC 09102
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Q9Z164
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96 EGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRLVKVSG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DGAPCIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFPRRVKLPG 60
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320 CCTPLOTRIVIMRFRCEDGEMFSKNVMMIQSCKCNVNCPHPNEASFRLY -- SLFNDI 374
                               62 CCTPHRITILPVEFKCPDGEIMKKUMMFIKICACHYNCPGDNDIFESLYYRKMYGDM 118
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91096871; PubMed=1756408;
MEDLINE=92096871; PubMed=1756408;
Martinerie C., Perbal B.;
Martinerie C., Perbal B.;
In human tissues.";
In human tissues.";
In R. Acad. Sci., III, Sci. Vie 313:345-351(1991),
InterPro; IPRO01007; VWF.C.
PROSITE; PS01208; VWFC_1;
PROSITE; PS01208; VWFC_1;
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                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Potential IGF binding protein (Fragments).
Endon sepiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.2%; Score 341; DB 4; Length 100;
Best Local Similarity 40.5%; Pred. No. 1e-24;
Matches 64; Conservative 15; Mismatches 21; Indels
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100 Aa; 10813 MW; C64EE2B9AD8A3299 CRC64;
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                                                                                                                                                                        PRT; 100 AA
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                                                                                                                                                                      PRELIMINARY;
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SEQUENCE
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C9UDL6
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